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OM protein - protein search, using sw model

Run on: February 24, 2006, 15:47:43 ; Search time 47 Seconds
(without alignments)
209.328 Million cell updates/sec

Title: US-10-751-451-2

Perfect score: 649

Sequence: 1 PLATROGKRPSKNLKARCSR.....ANNVYKQYEDMVVSCGCR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	645	99.4	119	2	US-09-068-253-2
2	645	99.4	120	1	US-08-362-670B-4
3	645	99.4	120	1	US-08-333-576C-4
4	645	99.4	120	2	US-08-808-324-4
5	645	99.4	120	2	US-09-945-182-4
6	645	99.4	120	4	PCT-US94-14030A-4
7	645	99.4	401	2	US-08-289-222E-3
8	645	99.4	401	2	US-09-054-526B-3
9	645	99.4	501	1	US-08-288-508C-2
10	645	99.4	501	2	US-08-981-490B-1
11	645	99.4	501	2	US-09-386-450D-2
12	645	99.4	501	2	US-09-949-016-5956
13	645	99.4	579	2	US-09-949-016-10132
14	640	98.6	119	1	US-08-455-559-13
15	640	98.6	119	2	US-09-145-060-13
16	640	98.6	119	4	PCT-US94-00657-13
17	640	98.6	495	1	US-08-455-559-10
18	640	98.6	495	2	US-09-145-060-10
19	640	98.6	495	4	PCT-US94-00657-10
20	559	86.1	102	1	US-08-335-583C-51
21	559	86.1	102	1	US-08-288-508C-13
22	559	86.1	102	2	US-08-289-222E-22
23	559	86.1	102	2	US-09-054-526B-22
24	559	86.1	102	2	US-09-374-958C-83
25	559	86.1	102	2	US-09-386-450D-13
26	559	86.1	102	2	US-09-374-936-83
27	543	83.7	119	1	US-08-581-529B-7

28 543 83.7 119 2 US-09-097-616-7 Sequence 7, Appli
29 543 83.7 119 2 US-09-619-061-7 Sequence 7, Appli
30 543 83.7 119 4 PCT-US94-07762-7 Sequence 7, Appli
31 543 83.7 134 1 US-08-581-529B-6 Sequence 6, Appli
32 543 83.7 134 2 US-09-097-616-6 Sequence 6, Appli
33 543 83.7 134 2 US-09-619-061-6 Sequence 6, Appli
34 543 83.7 134 4 PCT-US94-07762-6 Sequence 6, Appli
35 540 83.2 321 1 US-08-362-670B-26 Sequence 26, Appli
36 540 83.2 321 2 US-08-333-576C-26 Sequence 26, Appli
37 540 83.2 321 2 US-08-808-324-26 Sequence 26, Appli
38 540 83.2 321 2 US-09-945-182-26 Sequence 26, Appli
39 540 83.2 321 4 PCT-US94-14030A-26 Sequence 26, Appli
40 538 82.9 263 1 US-08-362-670B-32 Sequence 32, Appli
41 538 82.9 263 2 US-08-333-576C-32 Sequence 32, Appli
42 538 82.9 263 2 US-08-808-324-32 Sequence 32, Appli
43 538 82.9 263 2 US-09-945-182-32 Sequence 32, Appli
44 538 82.9 263 4 PCT-US94-14030A-32 Sequence 32, Appli
45 510 78.6 102 2 US-09-374-958C-85 Sequence 85, Appli

ALIGNMENTS

RESULT 1

US-09-068-253-2

; Sequence 2, Application US/09068253

; Patent No. 6903071

; GENERAL INFORMATION:

; APPLICANT: SHIMURA, Takesada

; APPLICANT: TORIYAMA, Sateuki

; TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION

; FILE REFERENCE: 146.1286

; CURRENT APPLICATION NUMBER: US/09/068.253

; CURRENT FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: PCT/JP96/03333

; PRIOR FILING DATE: 1996-11-14

; PRIOR APPLICATION NUMBER: JP 7/322402

; PRIOR FILING DATE: 1995-11-17

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 119

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-068-253-2

Query Match 99.4%; Score 645; DB 2; Length 119;

Best Local Similarity 99.2%; Pred. No. 2.5e-64;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATROGKRPSKNLKARCSRKALHVNFKMDWDWIAPLEYAFHCEGLCEFFPLRSHLE 60

Db 1 PLATROGKRPSKNLKARCSRKALHVNFKMDWDWIAPLEYAFHCEGLCEFFPLRSHLE 60

Qy 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119

Db 61 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119

RESULT 2

US-08-362-670B-4

; Sequence 4, Application US/08362670B

; Patent No. 5658882

; GENERAL INFORMATION:

; APPLICANT: Celeste, Anthony J.

; APPLICANT: Wozney, John

; APPLICANT: Rosen, Vicki A.

; APPLICANT: Wolfman, Neil

; APPLICANT: Thomsen, Gerald H.

; APPLICANT: Melton, Douglas A.

; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRPSKNLKARCSRKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
Db 2 PLATQGRPSKNLKARCSRKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 61

Qy 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVVKYEDMNVVSCGCR 119
Db 62 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKYEDMNVVSCGCR 120

RESULT 5
US-09-945-182-4
; Sequence 4, Application US/09945182
; Patent No. 6719968
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; Mooney, John
; Rosen, Vicki A.
; Wolfman, Neil
; Melton, Gerald H.
; Thomsen, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/945,182
; FILING DATE: 31-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,324
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-945-182-4

Query Match 99.4%; Score 645; DB 2; Length 120;
Best Local Similarity 99.2%; Pred. No. 2.5e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRPSKNLKARCSRKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
Db 2 PLATQGRPSKNLKARCSRKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 61

Qy 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVVKYEDMNVVSCGCR 119
Db 62 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKYEDMNVVSCGCR 120

RESULT 6

PCT-US94-14030A-4
; Sequence 4, Application PC/TUS9414030A
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14030A
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,103
; FILING DATE: 07-DEC-1993
; APPLICATION NUMBER: US 08/217,780
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 08/333,576
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202D-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-14030A-4

Query Match 99.4%; Score 645; DB 4; Length 120;
Best Local Similarity 99.2%; Pred. No. 2.5e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRPSKNLKARCSRKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
Db 2 PLATQGRPSKNLKARCSRKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 61

Qy 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVVKYEDMNVVSCGCR 119
Db 62 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKYEDMNVVSCGCR 120

RESULT 7
US-08-289-222E-3
; Sequence 3, Application US/08289222E
; Patent No. 6120760
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, GERTRUD
; APPLICANT: NEIDHARDT, HEUGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
; TITLE OF INVENTION: FAMILY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI DO, MARCELSTEIN, MURRAY & ORAM
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,

STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222E-3

Query Match 99.4%; Score 645; DB 2; Length 401;
Best Local Similarity 99.2%; Pred. No. 1.le-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKRLKARCSKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
DB 283 PLATQGRKPSKRLKARCSKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 342

QY 61 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 343 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 401

RESULT 8
US-09-054-526B-3
Sequence 3, Application US/09054526B
Patent No. 6157550
GENERAL INFORMATION:
APPLICANT: H TTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
SUITE 330
CITY: WASHINGTON
STATE: DC

COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-526B-3

Query Match 99.4%; Score 645; DB 2; Length 401;
Best Local Similarity 99.2%; Pred. No. 1.le-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKRLKARCSKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
DB 283 PLATQGRKPSKRLKARCSKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 342

QY 61 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 343 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 401

RESULT 9
US-08-288-508C-2
Sequence 2, Application US/08288508C
Patent No. 5994094
GENERAL INFORMATION:
APPLICANT: H Tten, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
THE TGF- FAMILY
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaïdo, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/288,508C
;; FILING DATE: 10-AUG-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DE P 43 26 829.3
;; FILING DATE: 10-AUG-1993
;; APPLICATION DATA:
;; APPLICATION NUMBER: DE P 44 18 222.8
;; FILING DATE: 25-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DE P 44 20 157.5
;; FILING DATE: 09-JUN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: JAHNS, Kristina M.
;; REGISTRATION NUMBER: P-41,092
;; REFERENCE/DOCKET NUMBER: P564-4019
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)638-5000
;; TELEFAX: (202)638-4810
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 501 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-288-508C-2

Query Match 99.4%; Score 645; DB 1; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.5e-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRPSKNLKARCSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
DB 383 PLATQGRPSKNLKARCSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442

QY 61 PTNHAVIOTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 443 PTNHAVIOTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 501

RESULT 10
US-08-981-490B-1
;; Sequence 1, Application US/08981490B
;; Patent No. 6531450
;; GENERAL INFORMATION:
;; APPLICANT: Hotten, Gertrud
;; APPLICANT: Pohl, Jens
;; APPLICANT: Bechtold, Rolf
;; APPLICANT: Paulista, Michael
;; APPLICANT: Unsicker, Klaus
;; TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
;; TITLE OF INVENTION: NERVOUS SYSTEM
;; FILE REFERENCE: 100564-07032
;; CURRENT APPLICATION NUMBER: US/08/981,490B
;; CURRENT FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: PCT/EP96/03065
;; PRIOR FILING DATE: 1996-07-12
;; PRIOR APPLICATION NUMBER: DE/195 25 416.3
;; PRIOR FILING DATE: 1995-07-12
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 501
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-08-981-490B-1

Query Match 99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.5e-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRPSKNLKARCSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
DB 383 PLATQGRPSKNLKARCSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442

QY 61 PTNHAVIOTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 443 PTNHAVIOTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 501

RESULT 11
US-09-386-450D-2
;; Sequence 2, Application US/09386450D
;; Patent No. 6764994
;; GENERAL INFORMATION:
;; APPLICANT: Hotten, Gertrud
;; APPLICANT: Neidhardt, Helge
;; APPLICANT: Paulista, Michael
;; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF TGF-? Family
;; FILE REFERENCE: 100564-09022
;; CURRENT APPLICATION NUMBER: US/09/386,450D
;; CURRENT FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: US 08/288,508
;; PRIOR FILING DATE: 1994-08-10
;; PRIOR APPLICATION NUMBER: DE P 43 26 829.3
;; PRIOR FILING DATE: 1993-08-10
;; PRIOR APPLICATION NUMBER: DE P 44 18 222.8
;; PRIOR FILING DATE: 1994-05-25
;; PRIOR APPLICATION NUMBER: DE P 44 20 157.5
;; PRIOR FILING DATE: 1994-06-09
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 501
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (1)..(501)
;; OTHER INFORMATION: TGF-beta protein MP-52 precursor
US-09-386-450D-2

Query Match 99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.5e-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRPSKNLKARCSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
DB 383 PLATQGRPSKNLKARCSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442

QY 61 PTNHAVIOTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 443 PTNHAVIOTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 501

RESULT 12
US-09-949-016-5956
;; Sequence 5956, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CLO01307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 5956
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5956

Query Match          99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.5e-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFLRSHLE 60
DB 383 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFLRSHLE 442

QY 61 PTNHAIVQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 443 PTNHAIVQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 501

RESULT 13
US-09-949-016-10132
; Sequence 10132, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10132
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10132

Query Match          99.4%; Score 645; DB 2; Length 579;
Best Local Similarity 99.2%; Pred. No. 1.8e-63;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFLRSHLE 60
DB 461 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFLRSHLE 520

QY 61 PTNHAIVQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 521 PTNHAIVQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 579

RESULT 14
US-08-455-559-13
; Sequence 13, Application US/08455559
; Patent No. 5801014
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLERY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,559
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/003,144
; FILING DATE: 12-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. PH.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: GDF-5
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
US-08-455-559-13

Query Match          98.6%; Score 640; DB 1; Length 119;
Best Local Similarity 98.3%; Pred. No. 8.9e-64;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFLRSHLE 60
DB 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFLRSHLE 60

QY 61 PTNHAIVQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 61 PTNHAIVQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119

RESULT 15
US-09-145-060-13
; Sequence 13, Application US/09145060
; Patent No. 6245896
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/145,060
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/455,559
; FILING DATE: 31-MAY-1995
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		Query Match	98.6%;	Score 640;	DB 2;	Length 119;
		Best Local Similarity	98.3%;	Pred. No. 8.9e-64;		
		Matches 117; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	PLATROGKPSKNLKARCSRKAALHVNFKMGWDWIIAPLEYEAFHCCEGLCEPPLASHLE	60			
Dd	1	PLANRQGKPSPKLNKARCSRKAALHVNFKMGWDWIIAPLEYEAFHCCEGLCEPPLASHLE	60			
Qy	61	PTNHAVIQTILMNSMDPESTPPTCVTRLSPIILFIDSANNVVYQYEDMVVESGCCR	119			
Dd	61	PTNHAVIQTILMNSMDPESTPPCTCVTRLSPIILFIDSANNVVYQYEDMVVESGCCR	119			

Search completed: February 24, 2006, 15:49:00
Job time : 47 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 15:40:14 ; Search time 185 Seconds
(without alignments)
282.627 Million cell updates/sec.

Title: US-10-751-451-2

Perfect score: 649

Sequence: 1 PLATQGRKPSKYLKRCR.....ANNVYQYEDMVESCCCR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	100.0	119	3	AAY44296 Mutant hu
2	645	99.4	119	2	Aaw06920 Human MP5
3	645	99.4	119	2	Aaw19846 Human bon
4	645	99.4	120	2	Aar78731 Murine pr
5	645	99.4	120	2	Aaw26590 Human MP5
6	645	99.4	120	4	Aae10973 Human MP5
7	645	99.4	120	6	ABg73290 Amino aci
8	645	99.4	401	2	Aar40800 TGF-beta-
9	645	99.4	501	2	Aar69600 New TGF-b
10	645	99.4	501	2	Aaw12770 Human bon
11	645	99.4	501	2	Aaw19210 Human MP5
12	645	99.4	501	2	Aaw36100 Human TGF
13	645	99.4	501	2	Aaw11900 Human hig
14	645	99.4	501	2	Aaw01799 Human MP5
15	645	99.4	501	2	Aaw4868 TGF-beta
16	645	99.4	501	2	Aaw33008 Human MP5
17	645	99.4	501	4	Aab70529 Human TGF
18	645	99.4	501	8	ADG14191 Human ful
19	645	99.4	501	8	Adm32627 Modified
20	645	99.4	501	8	Adm32624 Prepro fo
21	645	99.4	501	8	AdS97531 DNA encod
22	645	99.4	501	9	AdX15817 Human GDP
23	640	98.6	495	2	Aar60022 Growth di
24	640	98.6	495	4	Aab84550 Amino aci

25	640	98.6	495	6	ABG76018	Abg76018 Mouse gro
26	639	98.5	119	3	AAY70756	Aay70756 Methionin
27	639	98.5	119	3	AAY70758	Aay70758 Tryptopha
28	639	98.5	119	3	AAY70752	Aay70752 Wild type
29	639	98.5	119	3	AAY70757	Aay70757 Methionin
30	639	98.5	120	5	AAM51932	Aam51932 Human TGF
31	639	98.5	501	2	AAR95635	Aar95635 Cartilage
32	639	98.5	501	3	AAY92034	Aay92034 Human gro
33	633	97.5	120	8	ADH11614	Adh11614 Human bon
34	568	87.5	104	8	ADR05308	Adr05308 Human MP-
35	559	86.1	102	3	AAY92578	Aay92578 CDMP-1/GD
36	559	86.1	102	3	ABO9553	Aab09553 Human CDM
37	559	86.1	102	3	ABO2819	Aab02819 Human CDM
38	543	83.7	120	5	AAM51933	Aam51933 Murine TG
39	543	83.7	125	6	ABG76037	Abg76037 Human GDF
40	543	83.7	134	2	AAR66867	Aar66867 GDF-6..3/
41	543	83.7	134	3	AB112986	Aab112986 Murine gr
42	543	83.7	263	2	AAR78739	Aar78739 Murine mv
43	543	83.7	263	2	AAM26595	Aaw26595 Murine BM
44	540	83.2	120	8	ADH11613	Adh11613 Human bon
45	540	83.2	321	2	AAR78730	Aar78730 Human mat

ALIGNMENTS

RESULT 1

AAY44296

ID AAY44296 standard; protein; 119 AA.

XX AAY44296;

AC AAY44296;

XX AAY44296;

DT 29-FEB-2000 (first entry)

DE Mutant human MP52 monomer protein.

XX DE

XX DE

KW Mutant MP52 monomer protein; transforming growth factor-beta; TGF-beta;

KW PKOT279 expression vector; osteocyte; bone morphogenetic; osteopathic;

KW anti-arthritis activity; cartilage; osteoporosis; osteoarthritis;

KW arthrosclerosis; fracture; achondroplasia; dyschondrogenesis;

KW achondrogenesis; palatoschisis; dysosteogenesis.

XX OS Homo sapiens.

OS Synthetic.

XX OS

PH Key

FT Misc-difference 83

FT Location/Qualifiers

XX /note= "Wild-type Cys replaced by Ala"

XX WO9961611-Al.

XX 02-DEC-1999.

XX 14-MAY-1999; 99WO-IB0000866.

XX 22-MAY-1998; 98JP-00141379.

XX (HMRI) HOECHST MARION ROUSSEL LTD.

XX Kawai S, Kimura M, Muraki Y, Katsura M;

XX WPI; 2000-097122/08.

XX N-PSDB; AAZ29328.

XX Novel monomer protein used for prevention and treatment of bone and/or

XX cartilage diseases.

XX Claim 4; Page 20; 26pp; English.

XX The present sequence is a mutant human MP52 monomer protein, which

XX belongs to transforming growth factor-beta (TGF-beta) superfamily. Mutant

XX MP52 can be produced in E. coli cells by transforming them with PKOT279

XX expression vector containing a mutated MP52 monomer encoding nucleic acid

CC sequence. MP52 monomer protein is capable of inducing differentiation in
 CC osteocytes and exhibits bone morphogenetic, osteopathic and anti-
 CC arthritic activity. The MP52 monomer protein is used for prevention and
 CC treatment of cartilage and/or bone diseases such as osteoporosis,
 CC osteoarthritis, arthrosclerosis, damage of cartilage, regeneration of bone,
 CC cartilage deficit caused by injury and tumour dissection, fracture,
 CC congenital bone and/or cartilage diseases such as achondroplasia,
 CC dyschondrogenesis, achondrogenesis, palatoschisis and dysosteogenesis and
 CC a deficit of root of teeth and a tooth socket
 XX
 SQ Sequence 119 AA;

Query Match 100.0%; Score 649; DB 3; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.5e-59;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKALKARCSKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
 DB 1 PLATROGKRPSSKALKARCSKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
 QY 61 PTNHAVIOTLMSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
 DB 61 PTNHAVIOTLMSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119

RESULT 2
 AAW06920
 ID AAW06920 standard; protein; 119 AA.

XX AC AAW06920;

DT 27-JUN-1997 (first entry)

XX Human MP52 growth factor residues 383-501.

XX Human; MP52; growth factor; monomer; dimer; treatment; bone; cartilage;
 XX dental; disorder; fracture; bone loss; periodontal disease;
 XX calcification; osteoporosis.

XX OS Homo sapiens.

XX FN WO9633215-Al.

XX PD 24-OCT-1996.

XX PF 19-APR-1996; 96WO-JP001062.

XX PR 19-APR-1995; 95JP-00093664.

XX PR 17-NOV-1995; 95JP-00322403.

XX (FARH) HOECHST JAPAN LTD.

XX PI Makishima F, Takamata H, Miki H, Kawai S, Kimura M, Matsumoto T;

XX PI Katsura M, Enomoto K, Satoh Y;

XX WIPI; 1996-485730/48.

XX N-PSDB; AAT46150.

XX Peptide consisting of part of human MP52 growth factor, and its dimer -
 XX is used for treatment of bone, cartilage and dental disorders.

XX Claim 1; Page 18-19; 33pp; Japanese.

XX The present sequence is residues 383 to 501 of the human MP52 growth
 XX factor, a dimer of which can be used to treat bone, cartilage and dental
 XX disorders, including fractures, bone loss and periodontal disease. The
 XX dimer was prepared by transforming a host (preferably E. coli) with a
 XX suitable (plasmid) expression vector containing DNA encoding the monomer.
 XX The host was cultured, and inclusion bodies from the cells worked up to
 XX give the monomer, which was then converted into the dimer. The product
 XX was mixed with type 1 pig tendon collagen and injected into the large
 XX thigh vein of ICR mice. After 20 days, 4 of 4 mice injected with 10 microg
 XX of the dimer showed bone/cartilage calcification around the injection

CC site, compared to none in 0 of 4 mice treated with collagen only
 XX
 SQ Sequence 119 AA;

Query Match 99.4%; Score 645; DB 2; Length 119;
 Best Local Similarity 99.2%; Pred. No. 3.9e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKALKARCSKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
 DB 1 PLATROGKRPSSKALKARCSKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
 QY 61 PTNHAVIOTLMSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
 DB 61 PTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119

RESULT 3

AAW19846

ID AAW19846 standard; protein; 119 AA.

XX AC AAW19846;

DT 12-FEB-1998 (first entry)

XX Human bone inducing factor MP52.

XX Human; bone inducing factor; MP52; collagen; fracture;

XX polyoxyethylene-polyoxypropylene glycol.

XX OS Homo sapiens.

XX PN WO9718829-Al.

XX PD 29-MAY-1997.

XX PF 14-NOV-1996; 96WO-JP003333.

XX PR 17-NOV-1995; 95JP-00322402.

XX (FARH) HOECHST PHARM & CHEM KK.

XX Shimura T, Toriyama S;

XX WIPI; 1997-310243/28.

XX DR N-PSDB; AAT70296.

XX Material for repairing bone and collagen, especially bone fracture or
 XX loss - comprising bone-inducing factor and polyoxyethylene-
 XX polyoxypropylene glycol compounds.

XX Example 4; Page 16-17; 31pp; Japanese.

XX Bone and collagen inducing material has been developed which comprises
 XX bone inducing factor and polyoxyethylene-polyoxypropylene glycol
 XX compounds. The present sequence represents human bone inducing factor
 XX MP52. This material allows treatment without surgery. It is highly
 XX absorbable because a carrier is used with the bone inducing factor, and
 XX undergoes reversible sol-gel transition depending on the temperature

XX SQ Sequence 119 AA;

Query Match 99.4%; Score 645; DB 2; Length 119;
 Best Local Similarity 99.2%; Pred. No. 3.9e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKALKARCSKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
 DB 1 PLATROGKRPSSKALKARCSKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60

QY 61 PTNHAVIOTLMSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
 DB 61 PTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119

XX DE Human MP-52 protein.
XX DE Human; MP-52; vulnary; antiinflammatory; analgesic; ligament defect;
XX KW transforming growth factor-beta; TGF-beta; tissue formation; tendonitis;
XX KW wound healing; tissue repair; carpal tunnel syndrome; gene therapy.
XX OS Homo sapiens.
XX OS USG284872-B1.
XX FN 04-SEP-2001.
XX PD 28-FEB-1997; 97US-00808324.
XX PF 07-DEC-1993; 93US-00164103.
XX PR 25-MAR-1994; 94US-00217780.
XX PR 02-NOV-1994; 94US-00333576.
XX PR 22-DEC-1994; 94US-00362670.
XX (GEMY) GENETICS INST INC.
XX (HARD) HARVARD COLLEGE.
XX Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
XX Melton DA;
XX WPI; 2001-588978/66.
XX N-PSDB; AAD18317.
XX New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome
XX and other tendon and ligament defects, comprises DNA encoding propeptide
XX linked to DNA encoding bone morphogenetic proteins (BMP)-12, BMP-13 or
XX MP52.
XX Disclosure; Col 39-40; 42pp; English.
XX The invention relates to a chimeric DNA comprising a DNA sequence
XX encoding a propeptide from a member of the transforming growth factor
XX (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
XX encoding an amino acid sequence encoding a mature polypeptide consisting
XX of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA
XX sequences are useful for producing proteins which induce tendon/ligament
XX like tissue formation, and for isolating and cloning further DNA
XX sequences encoding BMP-12 related proteins with similar activity. The
XX proteins are useful for the induction of tendon/ligament-like tissue
XX formation, wound healing, ligament and other tissue repair, augmenting
XX the activity of bone morphogenetic proteins, and for treating tendonitis,
XX carpal tunnel syndrome and other tendon and ligament defects. The present
XX sequence is human MP-52 protein
XX Sequence 120 AA;
XX Query Match 99.4%; Score 645; DB 4; Length 120;
XX Best Local Similarity 99.2%; Pred. No. 3.9e-59;
XX Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLATRGKRPSPKXKARCSKALHVNFKDMGWDMMIIAPLEYAFHCEGLCFPLRSHLE 60
Db 2 PLATRGKRPSPKXKARCSKALHVNFKDMGWDMMIIAPLEYAFHCEGLCFPLRSHLE 61
QY 61 PTNHAIVQTLNMSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
Db 62 PTNHAIVQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 120
RESULT 7
ABG73290
ID ABG73290 standard; protein; 120 AA.
AC ABG73290;
XX DT 30-APR-2003 (first entry)
XX

DE XX Amino acid sequence for human MP52.
KW Human; bone morphogenetic protein-12; BMP-12; BMP-12 related protein;
KW BMP-13; Vt-1; BMP/TGF-beta/Vg-1 family; tissue repair; tendonitis;
KW tendon/ligament-like tissue formation; trauma induced tendon defect;
KW tendon/ligament-like tissue healing; tendon damage; ligament damage;
KW tendon fixation; ligament fixation; congenital; ligament defect;
KW cosmetic plastic surgery; vulnary; MP52.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX Region 1. .120
XX FT /note= "Specifically claimed in Claim 26"
XX FT 19. .120
XX FT /note= "Specifically claimed in Claim 26"
XX FN US2002160494-A1.
XX PD 31-OCT-2002.
XX PF 31-AUG-2001; 2001US-00945182.
XX PR 07-DEC-1993; 93US-00164103.
XX PR 25-MAR-1994; 94US-00217780.
XX PR 02-NOV-1994; 94US-00333576.
XX PR 22-DEC-1994; 94US-00362670.
XX PR 28-FEB-1997; 97US-00808324.
XX (CELESTE A J.
XX (WOZNEY J M.
XX (ROSE) ROSEN V A.
XX (WOLF) WOLFMAN N M.
XX (THOM) THOMSEN G H.
XX (MELT) MELTON D A.
XX Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
XX Melton DA;
XX WPI; 2003-238228/23.
XX N-PSDB; ABX11141.
XX New bone morphogenetic proteins (designated BMP-12) or related proteins,
XX useful for inducing tendon/ligament-like tissue formation in a patient,
XX or for tendon/ligament-like tissue healing or repair (e.g. for treating
XX tendonitis).
XX Claim 26; Page 21; 46pp; English.
XX The present invention relates to the isolation of human bone
XX morphogenetic protein-12 (BMP-12) protein and a BMP-12 related protein
XX (designated BMP-13 or Vt-1), and the polynucleotide sequences encoding
XX them. The novel BMPs are members of the BMP/TGF-beta/Vg-1 family of
XX proteins. BMP-12 and Vt-1 are characterised by their ability to induce
XX the formation of tendon/ligament-like tissue. The BMP-12 proteins of the
XX invention are useful for inducing tendon/ligament-like tissue formation
XX in a patient. They are particularly useful for tendon/ligament-like
XX tissue healing and tissue repair, e.g. for treating tendonitis, or other
XX tendon or ligament defects in a patient. The polynucleotide sequences
XX encoding the BMP-12 proteins are useful for inducing tendon/ligament-like
XX tissue formation in a patient, and for tendon/ligament-like tissue
XX healing and tissue repair. The BMP-12 polypeptide and polynucleotide
XX sequences may be used for preventing damage to tendon or ligament tissue,
XX to improve fixation of tendon or ligament to bone or other tissues, to
XX repair congenital or trauma induced tendon or ligament defects, and in
XX cosmetic plastic surgery for attachment or repair of tendons or
XX ligaments. The present sequence represents human MP52
XX Sequence 120 AA;
XX Query Match 99.4%; Score 645; DB 6; Length 120;
XX Best Local Similarity 99.2%; Pred. No. 3.9e-59;
XX Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKPSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFPPLRSHLE 60
 DB |||||
 QY 2 PLATROGKPSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFPPLRSHLE 61
 DB |||||
 QY 61 PTNHAVIQTLMNSMDPESTPPACVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 119
 DB |||||
 QY 62 PTNHAVIQTLMNSMDPESTPPCCVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 120
 DB |||||

RESULT 8

AAR40800
 ID AAR40800 standard; protein; 401 AA.

XX AC AAR40800;
 XX DT 25-MAR-2003 (revised)
 XX DT 11-FEB-1994 (first entry)
 DE TGF-beta-like clone MP-52 protein.
 XX Human; transforming growth factor; beta; TGF-beta; pharmaceutical; bone;
 KW cartilage; tooth; wound repair; immunosuppressor; organ transplant;
 KW cosmetic surgery; antibody; diagnosis.
 XX OS Homo sapiens.
 XX PN W09316099-A2.
 XX PD 19-AUG-1993.
 XX PF 12-FEB-1993; 93WO-EP000350.
 XX PR 12-FEB-1992; 92EP-00102324.
 XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 XX PI Neidhardt H, Hoetten G;
 XX WPI; 1993-272824/34.
 XX DR N-PSDB; AAQ47709.
 XX PT New transforming growth factor-beta family proteins and DNA - used in
 XX tissue and wound repair, in treatment of bone, cartilage and tooth
 XX defects, and antibodies for diagnosis.
 XX PS Claim 11; Page 19; 29pp; English.

CC The sequences given in AAR40800 and AAR45447 represent fragments of embryo
 CC and liver derived human transforming growth factor-beta (TGF-beta)
 CC respectively. The full length protein may be used in a pharmaceutical
 CC composition for the treatment of various bone, cartilage or tooth defects
 CC and in tissue and wound repair processes. These proteins may also be used
 CC as immunosuppressors in organ transplants and in cosmetic surgery.
 CC Antibodies raised against these proteins may be used for diagnostic
 CC purposes. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 401 AA;

Query Match 99.4%; Score 645; DB 2; Length 401;
 Best Local Similarity 99.2%; Pred. No. 1.7e-58;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKPSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFPPLRSHLE 60
 DB 283 PLATROGKPSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFPPLRSHLE 342
 QY 61 PTNHAVIQTLMNSMDPESTPPACVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 119
 DB 343 PTNHAVIQTLMNSMDPESTPPCCVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 401

RESULT 9

AAR69600

ID AAR69600 standard; protein; 501 AA.

XX AC AAR69600;
 XX DT 25-MAR-2003 (revised)
 XX DT 10-OCT-1995 (first entry)
 DE New TGF-beta family member - MP-52 protein sequence.

XX Transforming growth factor-beta family; mitogenic; differentiation;
 KW treatment; prevention; disease; bone; cartilage; connective tissue; skin;
 KW mucosa; epithelium; dental tissue; wound healing; osteoporosis;
 KW tissue regeneration; arthritis; ss.

XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Peptide 382
 FT /label= mature protein
 XX PN W09504819-A1.
 XX PD 16-FEB-1995.
 XX PF 09-AUG-1994; 94WO-EP002630.
 XX PR 10-AUG-1993; 93DE-04326829.
 XX PR 25-MAY-1994; 94DE-04418222.
 XX PR 09-JUN-1994; 94DE-04420157.

XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 XX PI Hoetten G, Neidhardt H, Paulista M;
 XX WPI; 1995-090897/12.
 XX DR N-PSDB; AAQ83695.

XX New DNA encoding a new member of the TGF beta family - and related
 XX vectors, host cells etc., has mitogenic and differentiation inducing
 XX activity, e.g. for treating or preventing diseases of bone and cartilage
 XX etc.
 XX Claim 6; Page 36; 51pp; German.

CC The amino acid sequence of a novel member of the transforming growth
 CC factor-beta (TGF-b) family named MP-52. The gene encodes a protein of 501
 CC amino acids (AA). The protein, or at least the mature protein, has
 CC mitogenic and/or differentiation inducing properties useful in the
 CC treatment or prevention of diseases of bone, cartilage, connective
 CC tissue, skin, mucosa, epithelium or dental tissue. The protein can also
 CC be used for wound healing and tissue regeneration e.g. in osteoporosis
 CC and arthritis. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 501 AA;

Query Match 99.4%; Score 645; DB 2; Length 501;
 Best Local Similarity 99.2%; Pred. No. 2.2e-58;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKPSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFPPLRSHLE 60
 DB 383 PLATROGKPSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFPPLRSHLE 442
 QY 61 PTNHAVIQTLMNSMDPESTPPACVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 119
 DB 443 PTNHAVIQTLMNSMDPESTPPCCVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 501

RESULT 10

AAM12770
 ID AAM12770 standard; protein; 501 AA.

XX

XX DT 08-MAY-1998 (first entry)
XX DE Human MP52.
XX KW Bone morphogenetic protein; BMP; processing enzyme; MP52; BMP-2; BMP-4;
XX KW BMP-6; BMP-7; bone formation; bone regeneration.
XX OS Homo sapiens.
XX PN WO9741250-A1.
XX PD 06-NOV-1997.
XX PF 28-APR-1997; 97WO-JP001474.
XX PR 30-APR-1996; 96JP-00130618.
XX PA (FARH), HOECHST PHARM & CHEM KK.
XX PI Takahashi M, Makishima F, Kimura M;
XX DR WPI; 1997-549748/50.
XX DR N-PSDB; AAT98191.
XX KW Production of mature bone morphogenetic protein - by treatment of
PT precursor protein with a processing enzyme such as furin either directly
PT or by expressing them both in the same host.
XX PS Example 1; Page 21-25; 34pp; Japanese.
XX CC The present sequence is MP52, which is a bone morphogenetic protein
CC (BMP). Mature BMP can be produced by directly adding a BMP processing
CC enzyme to a solution containing BMP precursor protein, or by transforming
CC an animal cell with expression vectors containing DNA encoding the enzyme
CC and precursor protein, culturing the transformant and isolating the
CC mature BMP from the culture. The method can be used to produce MP52, BMP-
CC 2, BMP-4, BMP-6 and BMP-7, which can be used to treat bone formation or
CC regeneration abnormalities
XX SQ Sequence 501 AA;
Query Match 99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 2.2e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLATQGGKPSKALKARCSKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFPPLRSHLE 60
Db 383 PLATQGGKPSKALKARCSKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFPPLRSHLE 442
QY 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 119
Db 443 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 501
RESULT 13
AAW11900
ID AAW11900 standard; protein; 501 AA.
XX AC AAW11900;
XX DT 28-OCT-1997 (first entry)
XX DE Human high mol. wt. protein MP52, a growth/differentiation factor.
XX KW Growth factor; differentiation; bone induction; osteoporosis; teeth;
KW tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;
KW wound healing; regeneration; skeletal disorder; fracture; dimer.
XX OS Homo sapiens.
XX PN WO9704095-A1.
XX

PD 06-FEB-1997.
XX DT 24-JUL-1996; 96WO-JP002065.
XX PR 24-JUL-1995; 95JP-00218022.
XX PA (FARH) HOECHST PHARM & CHEM KK.
XX PI Kimura M, Matsumoto T, Takahashi M, Kawai S, Fujino Y;
XX DR WPI; 1997-132636/12.
XX DR N-PSDB; AAT61412.
XX KW High molecular weight human MP52 growth or differentiation factor -
PT promotes bone induction, is useful for treatment and prevention of bone
PT disease.
XX PS Claim 1; Page 12-16; 25pp; Japanese.
XX CC AAW11900 is a high mol. wt. form of a human growth/differentiation factor
CC MP52. MP52 promotes bone induction and is useful for plastic
CC reconstructive surgery, cosmetic facial treatment, bone transplantation
CC and tooth implantation. It is also useful for the treatment and
CC prevention of disorders of bone formation, bone, cartilage, joint tissue,
CC skin, mucous membranes, nails or teeth; for wound treatment and tissue
CC regeneration; and for the treatment of skeletal disorders and fractures
XX SQ Sequence 501 AA;
Query Match 99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 2.2e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLATQGGKPSKALKARCSKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFPPLRSHLE 60
Db 383 PLATQGGKPSKALKARCSKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFPPLRSHLE 442
QY 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 119
Db 443 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 501
RESULT 14
AAW01799
ID AAW01799 standard; protein; 501 AA.
XX AC AAW01799;
XX DT 15-OCT-1997 (first entry)
XX DE Human MP52 protein.
XX KW Human; MP52; transforming growth factor; TGF; beta; medicament;
KW treatment; prevention; nervous system; disease; neuropathology; ageing.
XX OS Homo sapiens.
XX PN DE19525416-A1.
XX PD 16-JAN-1997.
XX PF 12-JUL-1995; 95DE-01025416.
XX PR 12-JUL-1995; 95DE-01025416.
XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX PI Hoetten G, Pohl J, Bechtold R, Paulista M, Unsicker K;
XX DR WPI; 1997-078343/08.
XX DR N-PSDB; AAT59405.
XX KW Medicaments contg. protein MP52 - useful for treating neurological

PT disorders.
XX Claim 2; Page 12-14; 21pp; German.
XX
XX The present sequence is the human MP52 protein, which is described in WO
CC 9316099 and 9504819 as a member of the human transforming growth factor
CC beta superfamily. Active MP52 can be used in a medicament to treat and
CC prevent nervous system diseases, and/or to treat neuropathological
CC conditions caused by nervous system ageing
XX
XX SQ Sequence 501 AA;

Query Match 99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 2.2e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 PLATRQGRPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
Db 383 PLATRQGRPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442
Qy 61 PTNHAVIQTLLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 443 PTNHAVIQTLLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 501

RESULT 15
AAW44868
ID AAW44868 standard; protein; 501 AA.
XX AC AAW44868;
XX
DT 24-SEP-1998 (first entry)
XX
DE TGF-beta superfamily subunit.
XX
KW TGF-beta; calcium phosphate matrix; bioactive implant; parodontosis;
KW bone replacement; cartilage; bone; fracture.
XX
OS Synthetic.
XX
XX DE19647853-A1.
XX
PD 20-MAY-1998.
XX
XX PF 19-NOV-1996; 96DE-01047853.
XX
XX PR 19-NOV-1996; 96DE-01047853.
XX
XX (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
PA (GERO-) GERONTOCARE GMBH BIOMATERIALS & MEDICAL.
XX
XX Paulista M, Pohl J, Pabst J, Heide H;
XX WPI; 1998-287890/26.
XX
XX Bioactive implant material for bone replacement - comprising osteogenic
PT calcium phosphate matrix coated with protein.
XX
XX Claim 3; Page 8-10; 12pp; German.
XX
XX The TGF-beta superfamily subunit can be used together with a calcium
CC phosphate matrix to produce a bioactive implant material for bone
CC replacement. The implant has cartilage and/or bone-forming activity and
CC can be used for local treatment of cartilage and/or bone diseases or
CC damage caused by trauma, surgery, degeneration or overloading. The
CC implant can also be used for the treatment of bone defects, e.g.
CC parodontosis or fractures and in cosmetic and plastic surgery for fixing
CC mobile bones
XX
XX SQ Sequence 501 AA;

Query Match 99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 2.2e-58;

Search completed: February 24, 2006, 15:43:30
Job time : 188 secs

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 383 PLATRQGRPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442
Qy 61 PTNHAVIQTLLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 443 PTNHAVIQTLLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 501

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OM protein - protein search, using sw model

Run on: February 24, 2006, 15:43:48 ; Search time 38 Seconds
(without alignments)
301.310 Million cell updates/sec

Title: US-10-751-451-2
Perfect score: 649
Sequence: 1 PLATQGRPSKNLKARCSR.....ANNVYKQYEDMVVESCGR 119
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	645	99.4	501	2 J23247	growth/differentia
2	640	98.6	495	2 S43294	bone morphogenetic
3	639	98.5	501	2 A5452	cartilage-derived
4	543	83.7	125	2 S43295	bone morphogenetic
5	528	81.4	436	2 B5452	cartilage-derived
6	493	76.0	151	2 S43296	bone morphogenetic
7	353.5	54.5	461	2 S52408	SPDVR1 protein - s
8	347	53.5	393	2 S37073	bone morphogenetic
9	347	53.5	394	2 S45355	bone morphogenetic
10	347	53.5	396	1 BMH2	bone morphogenetic
11	347	53.5	401	2 JH0689	bone morphogenetic
12	346	53.3	400	2 A49147	bone morphogenetic
13	346	53.3	405	2 I50608	bone morphogenetic
14	344	53.0	588	2 A26158	decapentaplegic pr
15	343	52.9	398	2 JH0688	bone morphogenetic
16	343	52.9	398	2 JH0687	bone morphogenetic
17	341	52.5	408	2 S38343	bone morphogenetic
18	341	52.5	420	2 I49541	bone morphogenetic
19	339	52.2	408	1 BMH4	bone morphogenetic
20	338	52.1	408	2 S58791	bone morphogenetic
21	337	51.9	353	2 I50607	bone morphogenetic
22	333	51.3	207	2 S37618	vgr protein - rat
23	333	51.3	452	2 I49542	bone morphogenetic
24	333	51.3	454	1 BMH5	bone morphogenetic
25	332	51.2	513	1 BMH6	bone morphogenetic
26	331	51.0	408	2 JH0801	bone morphogenetic
27	330	50.8	313	2 I51284	bone morphogenetic
28	330	50.8	431	1 BMH7	bone morphogenetic
29	329	50.7	510	2 A54798	Vg-1-related prote

30	328	50.5	426	2 JH0690	bone morphogenetic
31	327	50.4	430	2 JQ1184	osteogenic protein
32	317.5	48.9	402	2 A45056	osteogenic protein
33	313	48.2	360	2 A29619	Vgi embryonic grow
34	306.5	47.2	365	2 T43286	cat-1 protein - Ca
35	304	46.8	455	2 A43918	TGF-beta-related p
36	303	46.7	427	2 A40735	TGF beta homolog d
37	283.5	43.7	366	2 A46607	growth/differentia
38	281	43.3	472	1 BMH3	bone morphogenetic
39	279.5	43.1	360	2 I53032	bone morphogenetic
40	278.5	42.9	366	2 A45402	transforming growt
41	274	42.2	366	2 T03907	TGF-beta-related p
42	271.5	41.8	372	2 C39364	GDF-1 embryonic gr
43	268.5	41.4	476	2 JC4646	bone morphogenetic
44	264.5	40.8	357	2 A39364	GDF-1 embryonic gr
45	264.5	40.8	478	2 JC4838	bone morphogenetic

ALIGNMENTS

RESULT 1

JC2347
growth/differentiation factor 5 - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: JC2347
R:Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.
Biochem. Biophys. Res. Commun. 204, 646-652, 1994
A>Title: Cloning and expression of recombinant human growth/differentiation factor 5.
A:Reference number: JC2347; MUID:95071375; PMID:7980526
A:Accession: JC2347
A:Molecule type: DNA
A:Residues: 1-501 <HOE>
A:Cross-references: UNIPROT:P43026; UNIPARC:UPI0000002E33B; GB:X80915; NID:9671524; PIDN:
C:Genetics:
A:Gene: GDB:BMP9
A:Cross-references: GDB:433948
A:Introns: 211/1
A:Superfamily: inhibin
C:Keywords: Glycoprotein
F:185/Binding site: carbohydrate (asn) (covalent) #status predicted
F:381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match	99.4%	Score 645;	DB 2;	Length 501;
Best Local Similarity	99.2%	Pred. No. 8.2e-59;		
Matches 118;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	PLATQGRPSKNLKARCSRKALHVNFKDGMWDWIIAPLEYEAFHCEGLCEFFPLRSHLE	60	
Db	383	PLATQGRPSKNLKARCSRKALHVNFKDGMWDWIIAPLEYEAFHCEGLCEFFPLRSHLE	442	
Qy	61	PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILPIDSANNVYKQYEDMVVESCGR	119	
Db	443	PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILPIDSANNVYKQYEDMVVESCGR	501	

RESULT 2

S43294
bone morphogenetic protein-related protein (GDF5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S43294
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A>Title: Limb alterations in brachypodism mice due to mutations in a new member of the
A:Reference number: S43294; MUID:94195427; PMID:8145850
A:Accession: S43294
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <STO>
A:Cross-references: UNIPROT:P43027; UNIPARC:UPI00000001AAC; GB:U08337; NID:9488461; PIDN:
C:Superfamily: inhibin

Query Match 53.5%; Score 347; DB 2; Length 394;
Best Local Similarity 54.3%; Pred. NO. 3.9e-28;
Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQK-RPFSNLRKARSRKALHVNFKDMGDDWTIIAPLEYEAFCEGLCEPPLRSHLEPTN 63
DB 280 RQAKHKORGLKSSCKRHPLYVDVDSVGNDWTIVAPPGHYAFYCHGECPPPLADHLNSTN 339

QY 64 HAVVILMNWDFESIFFACVFKLTSFSLFIDSANNVWIRQIEMWVSCGCR 111

Db 340 HALVOTLVNSVN-SKIPKACCVPTLSAISMLYLDENEKVLKNYOMWVEGCGCR 394

RESULT 10
BMH02

N/Alternate names: bone morphogenetic protein 2A; INHBPZ
C/Species: Homo sapiens (man)
C/Date: 16-Sep-1992 #sequence revision 03-Aug-1995 #text change 09-Jul-2000

Science 242, 1528-1534, 1988

A;Molecule type: mKNA
A;Residues: 1-396 <W02>
A;Cross-references: UNIPROT:P12643; UNIPARC:U010000173383
R;Tshida, N.; Tsujimoto, M.; Kanaya, T.; J. Biochem. 115, 279-285, 1994
A;Title: Expression and characterization of the protein
A;Reference number: PC2178; MUID:94266754
A;Accession: PC2178
A;Molecule type: protein
A;Residues: 230-295, X' 297-304 <ISH>
A;Cross-references: UNIPARC:U010000173383
A;Experimental source: cell line BOMo-15A
R;Rathore, S.; Hammerstone, K.M.; Dansereau, Protein Sci. 4(Suppl.2), 443S, 1995
A;Title: N-terminal isoforms of recombinant protein
A;Reference number: A56729
A;Contents: annotation

C;Comment: This hormone is capable of inducing bone formation at ectopic m
C;Genetics:

A; Map position: 20p12-20p12
C; Complex: homodimer, disulfide linked

F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-265/Domain: propeptide #status predicted <PRO>

F;135,164,200/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;283/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

	Query Match	Best Local Similarity	Score
· Matches	63; Conservative	54.3%;	53.5%;
			Pred. NC; Mismatches 17;
Qy	5	RQK-RPSKILKARCSRKALHVNFKDMQK	
Db	282	RQKHQRKRLKSSCKRHPLVDFSDV	
Qy	64	HAVIQTLNNSMDPSTPTTACVPTRLSL	
Db	342	HAVIQTLNNSVN-SKIPKACVPTRLSL	

RESULT 15

JH0688
bone morphogenetic protein 2II precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JH0688
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
A:Reference number: JH0687; MUID:92378616; PMID:1510675
A:Accession: JH0688
A:Molecule type: mRNA
A:Residues: 1-398 <NIS>
A:Cross-references: UNIPROT:P30884; UNIPARC:UPI00000000DAC; GB:X63425; NID:G64583; PIDN:C
A:Experimental source: oocyte
C:Superfamily: inhibin
C:Keywords: glycoprotein
F:285-398/Product: bone morphogenetic protein 2II #status predicted <MAT>
F:137,202,237,340/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 52.9%; Score 343; DB 2; Length 398;
Best Local Similarity 53.4%; Pred. No. 1e-27;
Matches 62; Conservative 19; Mismatches 33; Indels 2; Gaps 2;
QY 5 RQK-RPSKVLKARSRKALHVNFKDMGWDHIIAPLEYEAHCEGLCEFPPLRSHLEPTN 63
DB 284 ROARKQKRLKSSCRRLHYVDFSDVGWWDIVAPPGYHAFYCHGECFPPLADHLNSTN 343
QY 64 HAVIOTLMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMWVESCGR 119
DB 344 HAVIOTLMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMWVESCGR 398

Search completed: February 24, 2006, 15:48:07
Job time : 38 secs

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OM protein - protein search, using sw model

Run on: February 24, 2006, 15:40:18 ; Search time 230 Seconds
(without alignment)
365.034 Million cell updates/sec

Title: US-10-751-451-2

Perfect score: 649

Sequence: 1 PLATROGKRPSKNLKARCSR.....ANNVYKQYEDMVESGCR 119

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	645	99.4	501	1 GDF5 HUMAN	P43026 homo sapien
2	640	98.6	249	2 QBRW9 MOUSE	Q8brw9 mus musculus
3	640	98.6	495	1 GDF5 MOUSE	P43027 mus musculus
4	637	98.2	500	2 QW6G0 CHICK	Q9w6g0 gallus galli
5	611	94.1	494	2 Q68KG0 XENLA	Q68kg0 xenopus lae
6	587	90.4	324	2 Q9YHW9 CHICK	Q9yhw9 gallus galli
7	563	86.7	257	2 Q42303 BRARE	O42303 brachydanio
8	547	84.3	353	2 Q4SSW6 TETNG	Q4ssw6 tetraodon n
9	544	83.8	452	2 Q6HA10 RAT	Q6ha10 rattus norv
10	543	83.7	125	1 GDF6 MOUSE	P43028 mus musculus
11	543	83.7	454	2 Q7OUT4 MOUSE	Q7out4 mus musculus
12	540	83.2	201	2 Q6P158 HUMAN	Q6pi58 homo sapien
13	540	83.2	455	2 Q6KF10 HUMAN	Q6kfi10 homo sapien
14	534.5	82.4	126	2 Q93573 CHICK	Q93573 gallus galli
15	528	81.4	436	1 GDF6 BOVIN	P55106 bos taurus
16	527.5	81.3	261	2 Q9W6C0 BRARE	Q9w6c0 brachydanio
17	527	81.2	413	2 Q9DGN4 XENLA	Q9dgn4 xenopus lae
18	524	80.7	399	2 Q9W753 XENLA	Q9w753 xenopus lae
19	524	80.7	412	2 Q12938 BRARE	O12938 brachydanio
20	494	76.1	450	1 GDF7 HUMAN	Q7z4p5 homo sapien
21	494	76.1	453	2 Q75RY1 HUMAN	Q75ry1 homo sapien
22	493	76.0	461	1 GDF7 MOUSE	P43029 mus musculus
23	493	75.7	294	2 Q9BDW9 MACFA	Q9bdw9 macaca fasc
24	491	75.7	447	1 GDF7 CERAE	Q9bdw8 cercopithec
25	444	68.4	227	2 Q5KSY1 RAT	Q5ksy1 rattus norv
26	429	66.1	312	2 Q4TAX9 TETNG	Q4tax9 tetraodon n
27	368.5	56.8	361	2 Q96504 BRAFL	O96504 brachiosteo
28	368	56.7	204	2 Q9XZ69 TRIGR	Q9xz69 tripeustes
29	366	56.4	411	2 Q9U418 BRARE	Q9u418 brachiosteo
30	365	56.2	405	2 Q9U5E8 9BILA	Q9u5e8 ptychodera
31	363	55.9	229	2 Q4TAX8 TETNG	Q4tax8 tetraodon n

32	363	55.9	310	2	Q58G88 9ECHI	Q58g88 amphiuira fi
33	361	55.6	289	2	Q9XYQ8 STRPU	Q9xyq8 strongyloce
34	359	55.3	370	2	Q869A4 ACHTE	Q869a4 achaearanae
35	359	55.3	417	2	Q9XYQ7 LYTVA	Q9xyq7 lytechinus
36	357.5	55.1	509	2	Q8WS99 9ECHI	Q8ws99 archaster t
37	357	55.0	178	2	Q8K4X5 RAT	Q8k4x5 rattus norv
38	355.5	54.8	178	2	Q25211 JUNCO	Q25211 junonia coe
39	355.5	54.8	461	2	Q8MX23 HEMPU	Q8mx23 hemicentrot
40	354.5	54.6	435	2	Q5YJC3 9CNID	Q5yjc3 nematostell
41	354	54.5	67	2	Q02783 BOVIN	Q02783 bos taurus
42	353.5	54.5	461	1	DVRL1 STRPU	P48969 strongyloce
43	352	54.2	360	2	Q5TOL6 ANOGA	Q5tol6 anopheles g
44	352	54.2	379	2	Q6PUC6 ANOGA	Q6puc6 anopheles g
45	352	54.2	379	2	Q7Q3Q7 ANOGA	Q7q3q7 anopheles g

ALIGNMENTS

RESULT 1
ID GDF5 HUMAN STANDARD; PRT; 501 AA.
AC P43026; Q96SB1;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Growth/differentiation factor 5 precursor (GDF-5) (Cartilage-derived morphogenetic protein 1) (CDMP-1).
GN Name=GDF5; Synonyms=CDMP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=95071375; PubMed=7980526;
RA Hoetten G., Neidhardt H., Jacobowsky B., Pohl J.;
RT "Cloning and expression of recombinant human growth/differentiation factor 5";
RL Biochem. Biophys. Res. Commun. 204:646-652(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P., Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
RT "Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development.";
RL J. Biol. Chem. 269:28227-28234(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.T., Heath P.D., Ho S., Holden J.E., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.N., King A., Knights A., Laird G.K., Lawlor S., Leharvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie I.J., McLeay K., McMurray A.A., Milne S.A., Misry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rameay H.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20";
RL Nature 414:865-871(2001).
[4]
RP FNCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX TISSUE=Brain;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RP VARIANT CHODRODYSPLASIA TYR-400.
RX MEDLINE=97434212; PubMed=9288098;
RA Thomas J.T., Kilpatrick M.W., Lin K., Erlacher L., Lembessis P.,
RA Costa T., Tsiouras P., Luyten F.P.;
RT "Disruption of human limb morphogenesis by a dominant negative
RT mutation in CDMP1";
RL Nat. Genet. 17:58-64(1997).
[6]
RP MEDLINE=22117167; PubMed=12121354;
RA Fayaz-Ul-Haque M., Ahmad W., Zaidi S.H.E., Haque S., Tesbi A.S.,
RA Ahmad M., Cohn D.H., Tsui L.-C.;
RT "Mutation in the cartilage-derived morphogenetic protein-1 (CDMP1)
RT gene in a kindred affected with fibular hypoplasia and complex
RT brachydactyly (Dupan syndrome)";
RL Clin. Genet. 61:454-458(2002).
CC -!- FUNCTION: Could be involved in bone formation.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- TISSUE SPECIFICITY: Predominantly expressed in long bones during
CC human embryonic development.
CC -!- DISEASE: Defects in GDF5 are the cause of chondrodysplasia Grebe
CC type [MIM:200700]. Chondrodysplasia Grebe type is an autosomal
CC recessive disorder of limb development. It exhibits increasing
CC severity in a proximo-distal gradient and is therefore classified
CC as an acromesomelic dysplasia. The phenotype is characterized by a
CC normal axial skeleton, relatively normal humeri and femora, short
CC and deformed radii/ulnae and tibiae/fibulae, and severe
CC abnormalities of hands and feet. The digits are reduced to
CC globular appendages, and hexadactyly is common.
CC -!- DISEASE: Defects in GDF5 are the cause of acromesomelic
CC chondrodysplasia of the Hunter-Thompson type [MIM:201250]. This
CC form of dwarfism is characterized by short forearms, hands and
CC feet. The radius is curved and its head is often dislocated
CC posteriorly. The metacarpals, metatarsals and phalanges are
CC particularly short. The phalanges are almost square.
CC -!- DISEASE: Defects in GDF5 are the cause of brachydactyly type C
CC (BDC) [MIM:113100]. BDC is an autosomal dominant disorder
CC characterized by an abnormal shortness of the fingers and toes.
CC -!- DISEASE: Defects in GDF5 are the cause of Dupan syndrome

[MIM:228900]; also known as fibular hypoplasia and complex
brachydactyly. Dupan syndrome is a rare autosomal recessive
condition characterized by absence of the fibulae and severe
acromesomelic limb shortening with small, non-functional toes.
Although milder, the phenotype resembles the autosomal recessive
Hunter-Thompson [MIM:201250] and Grebe types [MIM:200700] of
acromesomelic chondrodysplasia.
-!- SIMILARITY: Belongs to the TGF-beta family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; X80915; CAA56874.1; -; Genomic_DNA.
CC EMBL; U13660; AAA57007.1; -; mRNA.
CC EMBL; AL21586; CAB89416.1; -; Genomic_DNA.
CC EMBL; BC032495; AAH32495.1; -; mRNA.
CC PIR; A55452; A55452.
CC PIR; JC2347; JC2347.
CC PDB; 1WAQ; X-ray; A=--.
CC PDB; 2BHK; X-ray; A=382-501.
CC SMR; P43026; 397-501.
CC Ensembl; ENSG00000125965; Homo sapiens.
CC HGNC; HGNC:4220; GDF5.
CC MIM; 601146; -.
CC MIM; 200700; -.
CC MIM; 201250; -.
CC MIM; 113100; -.
CC MIM; 228900; -.
CC GO; GO:0008083; F:growth factor activity; TAS.
CC GO; GO:0005515; F:protein binding; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0007179; P:transforming growth factor beta receptor si. .; TAS.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR001839; TGFb.
CC InterPro; IPR001111; TGFb_N.
CC Pfam; PF00019; TGF_beta; 1.
CC Pfam; PF00688; TGFb_propeptide; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRODOM; PD000357; TGFb; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC 3D-structure; Cytokine; Disease mutation; Dwarfism; Glycoprotein;
KW Growth factor; signal.
FT SIGNAL 1 27 Potential.
FT PROPEP 28 381 Potential.
FT CHAIN 382 501 Growth/differentiation factor 5.
FT CARBOHYD 189 189 N-linked (GlcNAc...) (Potential).
FT DISULFID 400 466 By similarity.
FT DISULFID 429 498 By similarity.
FT DISULFID 433 500 By similarity.
FT DISULFID 465 465 Interchain (By similarity).
FT DISULFID 400 400 C -> Y (in chondrodysplasia; Grebe type).
FT VARIANT 441 441 /FTid=VAR_017407.
FT VARIANT 441 441 L -> P (in Dupan syndrome).
FT VARIANT 38 38 /FTid=VAR_017408.
FT CONFLICT 254 258 T -> S (in Ref. 2).
FT CONFLICT 276 276 APGGG -> VPRSR (in Ref. 2).
FT CONFLICT 321 321 S -> A (in Ref. 2).
FT CONFLICT 321 321 A -> T (in Ref. 2).
FT CONFLICT 384 384 L -> S (in Ref. 2).
FT SEQUENCE 501 AA; 55411 MW; 37985F2D15C4F5EF CRC64;
Query Match 99.4%; Score 645; DB 1; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.5e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLATQGRPSKNLKARCSRKALVNFKMGWDDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
Db 383 PLATQGRPSKNLKARCSRKALVNFKMGWDDWIIAPLEYAFHCEGLCEFFPLRSHLE 442
QY 61 PTNHAIVQTLNMSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMWVSCGCR 119

DB 443 PTNHAIVOTLNSMDPESTPTCCVPTLSPISILFIDSANNVYKQYEDMWVSCGCR 501

RESULT 2

Q8BRW9 MOUSE

ID Q8BRW9_MOUSE PRELIMINARY; PRT; 249 AA.

AC Q8BRW9;

DT 01-MAR-2003 (TRENBLrel. 23, Created)

DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length

DE enriched library, clone:AS30087D05 product: growth differentiation

DE factor 5, full insert sequence. (fragment).

GN Name=Gdf5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;

RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Kiyosawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;

RA The FANTOM Consortium,

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;

RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;

RX MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multiplexed sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanganaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kotima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the TGF-beta family.

DR EMBL; AK041168; BAC30847.1; -; mRNA.

DR HSSP; P12643; 3BMP.

DR MGI; Q8BRW9; 145-249.

DR MGI; MGI-95688; Gdf5.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0030326; P:embryonic limb morphogenesis; IMP.

DR GO; GO:0042981; P:regulation of apoptosis; IMP.

DR InterPro; IPR002400; GF_cysknot.

DR InterPro; IPR002405; Inhibin_alpha.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR Pfam; PF00019; TGF_beta; 1.

DR PRINTS; PR00438; GFCVSKNOT.

DR PRINTS; PR00659; INHIBINA.

DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

KW Growth factor.

FT NON TER 1

SQ SEQUENCE 249 AA; 28409 MW; EGGA047F06B57189 CRC64;

Query Match 98.6%; Score 640; DB 2; Length 249;

Best Local Similarity 98.3%; Pred. No. 2.3e-59;

Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATQGRPSKLNKARCSKALHVNFKMGWDDWIIAPLEAEPHCGLCFFPLRSHLE 60

DB 131 PLANRQGRPSKLNKARCSKALHVNFKMGWDDWIIAPLEAEPHCGLCFFPLRSHLE 190

QY 61 PTNHAIVOTLNSMDPESTPTCCVPTLSPISILFIDSANNVYKQYEDMWVSCGCR 119

DB 191 PTNHAIVOTLNSMDPESTPTCCVPTLSPISILFIDSANNVYKQYEDMWVSCGCR 249

RESULT 3

GDF5 MOUSE

ID GDF5_MOUSE STANDARD; PRT; 495 AA.

AC P43027;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Growth/differentiation factor 5 precursor (GDF-5).

DE Name=Gdf5; Synonyms=Bp, Gdf-5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CD-1; TISSUE=Embryo;
RC MEDLINE=94195427; PubMed=8145850; DOI=10.1038/368639a0;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Lee S.-J.,
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF beta-superfamily.";
RL Nature 368:639-643(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Could be involved in bone formation.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- DISEASE: Defects in Gdf5 are the cause of brachypodism (bp) which
CC alters the length and numbers of bones in the limbs but spares the
CC axial skeleton.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U08337; AA18778.1; -; mRNA.
DR EMBL; BC034546; AAH34546.1; -; mRNA.
DR PIR; S43294; S43294.
DR HSSP; P12643; 3BMP.
DR SMR; P43027; 391-495.
DR Ensembl; ENSMUSG0000038259; Mus musculus.
DR MGI; MGI:95688; Gdf5.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005515; F:protein binding; IPL.
DR GO; GO:0030326; P:embryonic limb morphogenesis; IMP.
DR GO; GO:0042981; P:regulation of apoptosis; IMP.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Cytokine; Glycoprotein; Growth factor; Polymorphism; Signal.
FT SIGNAL 1 27 Potential.
FT PROPEP 28 375 Potential.
FT CHAIN 376 495 Growth/differentiation factor 5.
FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
FT DISULFID 394 460 By similarity.

FT DISULFID 423 492 By similarity.
FT DISULFID 427 494 By similarity.
FT DISULFID 459 459 Interchain (By similarity).
FT VARIANT 98 98 S -> P.
SQ SEQUENCE 495 AA; 54885 MW; CD0D5DE48185D2E3 CRC64;
Query Match 98.6%; Score 640; DB 1; Length 495;
Best Local Similarity 98.3%; Pred. No. 5.1e-59;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 PLATROGKRPSKNLKARCSRKALHNVFKDGMWDWIIAPLEYAFHCEGLCEFFPLRSLSLE 60
Db 377 PLANRQGRPSKNLKARCSRKALHNVFKDGMWDWIIAPLEYAFHCEGLCEFFPLRSLSLE 436
Qy 61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMNVVSCGCR 119
Db 437 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMNVVSCGCR 495
RESULT 4
Q9W6GU CHICK PRELIMINARY; PRT; 500 AA.
ID Q9W6GU; CHICK
AC Q9W6GU;
DT 01-NOV-1999 (TrEMBLrel. 12; Created)
DT 01-NOV-1999 (TrEMBLrel. 12; Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26; Last annotation update)
DE GDF-5 protein.
GN Name=gdf5;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=99146893; PubMed=10021348;
RX Francis-West P.H., Abdelfattah A., Chen P., Allen C., Parish J.,
RA Lader R., Allen S., Macpherson S., Luyten P., Archer C.W.;
RT "Mechanisms of GDF-5 action during skeletal development.";
RL Development 126:1305-1315(1999).
DR EMBL; AF123389; AAD30451.1; -; mRNA.
DR HSSP; P12643; 3BMP.
DR Ensembl; ENSGALG00000001786; Gallus gallus.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0040007; P:growth; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 500 AA; 55952 MW; 1DE8385A3119A598 CRC64;
Query Match 98.2%; Score 637; DB 2; Length 500;
Best Local Similarity 97.5%; Pred. No. 1.1e-58;
Matches 116; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 PLATROGKRPSKNLKARCSRKALHNVFKDGMWDWIIAPLEYAFHCEGLCEFFPLRSLSLE 60
Db 382 PLATROGKRPSKNLKARCSRKALHNVFKDGMWDWIIAPLEYAFHCEGLCEFFPLRSLSLE 441
Qy 61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMNVVSCGCR 119
Db 442 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMNVVSCGCR 500
RESULT 5

CC	-1- SIMILARITY: Belongs to the TGF-beta family.
DR	EMBL; AF075441; AAD14568.1; -, mRNA.
DR	HSSP; P08476; INYX.
DR	SMR; Q9YHW9; 229-324.
DR	EnsembI; ENSGALG0000001786; Gallus gallus.
DR	GO; GO:0005576; C:extracellular region; IEA.
DR	GO; GO:0008083; F:growth factor activity; IEA.
DR	GO; GO:0040007; P:growth; IEA.
DR	InterPro; IPRO02405; Inhibin_alpha.
DR	InterPro; IPRO01839; TGFB.
DR	InterPro; IPR001111; TGFb_N.
DR	Pfam; PF00688; TGFb_propeptide; 1.
DR	Pfam; PF00019; TGF_beta; 1.
DR	PRINTS; PR00669; INHIBINA.
DR	Prodrom; PD000357; TGFB; 1.
DR	SMART; SM00204; TGFB; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
KW	Growth factor. 1
FT	NON TER 1
FT	NON TER 324 324
SQ	SEQUENCE 324 AA; 37206 MW; OB8AYCB11375007 CRC64;
	Query Match 90.4%; Score 587; DB 2; Length 324;
	Best Local Similarity 97.3%; Pred.No.1.3e-53;
	Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0
QY	1 PLATQGKRPESKNLKARCSRKALHVNFKMGWDWIIAPLEYEAHPCEGLCFPLRSHLE 60
DB	215 PLATQGKRPESKNLKARCSRKALHVNFKMGWDWIIAPLEYEAHPCEGLCFPLRSHLE 274
QY	61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYED 110
DB	275 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEE 324
RESULT 7	
ID	O42303 BRARE PRELIMINARY; PRT; 257 AA.
AC	O42303;
DT	01-JAN-1998 (TREMBLrel. 05, Created)
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Contact (fragment).
GN	Name=gdf5;
OS	Brachydanio rerio (zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.
OX	NCBI TaxID=7955;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=97398455; PubMed=9256353; DOI=10.1016/S0925-4773(97)00072-5;
RA	Bruneau S., Mourrain P., Rosa F.M.;
RT	"Expression of contact, a new zebrafish DVR member, marks mesenchymal
RT	cell lineages in the developing pectoral fins and head and is
RT	regulated by retinoic acid.";
RL	Mech. Dev. 65:163-173(1997).
CC	-1- SIMILARITY: Belongs to the TGF-beta family.
CD	EMBL; Y12005; CRA72733.1; -; Genomic_DNA.
DR	HSSP; P08476; INYU.
DR	SMR; O42303; 153-257.
DR	EnsembI; ENSDARGO0000002760; Danio rerio.
DR	ZFIN; ZDB-GENE-990415-39; gdf5.
DR	GO; GO:0005576; C:extracellular region; IEA.
DR	GO; GO:0008083; F:growth factor activity; IEA.
DR	InterPro; IPRO02400; GF_cysknott.
DR	InterPro; IPRO02405; Inhibin_alpha.
DR	InterPro; IPRO01839; TGFB.
DR	Pfam; PF00019; TGF_beta; 1.
DR	PRINTS; PR00438; GFCYSKNOT.
DR	PRINTS; PR00669; INHIBINA.
DR	Prodrom; PD000357; TGFB; 1.
DR	SMART; SM00204; TGFB; 1.

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DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT CHAIN 140 257 Potential.
FT NON_TER 1 1
SQ SEQUENCE 257 AA; 29787 MW; 6D64F0542F948849 CRC64;

Query Match 86.7%; Score 563; DB 2; Length 257;
Best Local Similarity 86.0%; Pred. No. 3.4e-51;
Matches 98; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 6 QGKRPKNLKCRCRKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHA 65
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 144 RGKPIKPKQKCRNKRQLHVNFKMGWDDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHA 203

QY 66 VIOTLNMNDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 204 IIOTLNMNDPESTPTTCCVPTRLSPISILYIDSANNVYKQYEDMVVESCGR 257

RESULT 8
QASSW6_TETNG PRELIMINARY; PRT; 353 AA.
AC Q4SSW6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 8 SCAF14344, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00013233001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygia; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Maucell E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Dathouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brotier P., Coutureau J.P., Guzy J.,
RA Farra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SIMILARITY: Belongs to the TGF-beta family.
CC EMBL; CAAG01014344; CAF96266.1; -; Genomic_DNA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCVSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT NON_TER 1 1
SQ SEQUENCE 353 AA; 40336 MW; 04C3630767AF4124 CRC64;

Query Match 83.8%; Score 544; DB 2; Length 452;
Best Local Similarity 79.7%; Pred. No. 6.8e-49;
Matches 94; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 2 LATQGRKPSKNLKCRCRKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEPLRSHLEP 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 335 LSSRHGRKRGKSKRSRKLHVNFKELGWDWIIAPLEYEAFHCEGLCEPLRSHLEP 394

QY 62 TNHAVIOTLNMNDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 395 TNHAVIOTLNMNDPESTPTTCCVPTRLSPISILYIDSANNVYKQYEDMVVESCGR 452

RESULT 10
GDF6_MOUSE PRELIMINARY; PRT; 125 AA.
AC P43028;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
GN Name=Gdf6; Synonyms=Gdf-6;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Lee S.-J.;
 RT "Limb alterations in brachypodism mice due to mutations in a new
 member of the TGF beta-superfamily.";
 RL Nature 368:639-643(1994).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; U08338; AA18779.1; -; Unassigned_DNA.
 DR PIR; S43295; S43295.
 DR HSP; P08476; INYU.
 DR SMR; P43028; 21-125.
 DR Ensemble; ENSMUSG00000051279; Mus musculus.
 DR MGI; MGI:95689; Gdf6.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF_beta; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR00669; INHIBINA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Cytokine; Growth factor.
 FT PROPEP <1 5 Potential.
 FT CHAIN 6 125 Growth/differentiation factor 6.
 FT DISULFID 24 90 By similarity.
 FT DISULFID 53 122 By similarity.
 FT DISULFID 57 124 By similarity.
 FT DISULFID 89 89 Interchain (By similarity).
 FT NON_TER 1 1
 SQ SEQUENCE 125 AA; 14374 MW; 10FA2A5B7748DA32 CRC64;
 Query Match 83.7%; Score 543; DB 1; Length 125;
 Best Local Similarity 80.3%; Pred. No. 1.9e-49;
 Matches 94; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 OY 3 ATROGKPSKMLKARCSKALHVNFKMGWDDWIITAPLEYAFHCEGLCEPLRSHLPT 62
 DB 9 ASRHGKRGKSLRCSRKLPHVNFKELGWDDWIITAPLEYAFHCEGLCEPLRSHLPT 68
 OY 63 NHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 69 NHAIIQTLMNSMDPGSTPPCCVPTKLTPIISILYIDAGNNVYKQYEDMVVSCGCR 125
 RESULT 11
 ID Q70UT4_MOUSE PRELIMINARY; PRT; 454 AA.
 AC Q70UT4_MOUSE
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Growth differentiation factor 16.
 GN Name=Gdf6; Synonyms=GDF16;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Kunming; TISSUE=Brain;
 RA Guo J.H.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ537425; CAD60935.1; -; mRNA.
 DR HSP; P01137; IKLA.
 DR SMR; Q70UT4; 350-454.
 DR MGI; MGI:95689; Gdf6.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0040007; P:growth; IEA.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR Pfam; PF00019; TGF_beta; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR00669; INHIBINA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 SQ SEQUENCE 454 AA; 50941 MW; 5A3FADDA539CCB38 CRC64;
 Query Match 83.7%; Score 543; DB 2; Length 454;
 Best Local Similarity 80.3%; Pred. No. 8.8e-49;
 Matches 94; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 OY 3 ATROGKPSKMLKARCSKALHVNFKMGWDDWIITAPLEYAFHCEGLCEPLRSHLPT 62
 DB 338 ASRHGKRGKSLRCSRKLPHVNFKELGWDDWIITAPLEYAFHCEGLCEPLRSHLPT 397
 OY 63 NHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 398 NHAIIQTLMNSMDPGSTPPCCVPTKLTPIISILYIDAGNNVYKQYEDMVVSCGCR 454
 RESULT 12
 ID Q6PI58_HUMAN PRELIMINARY; PRT; 201 AA.
 AC Q6PI58;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE GDF6 protein (Fragment).
 GN Name=GDF6;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Stachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Maman A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; BC043222; AAH43222.1; -, mRNA.
DR HSP; P01137; IKLA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR Pfam; PF00019; TGF_beta.1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT NON_TER
SQ SEQUENCE 201 AA; 22441 MW; FF1ELD52BEE0517A CRC64;

Query Match 83.2%; Score 540; DB 2; Length 201;
Best Local Similarity 79.5%; Pred. No. 6.9e-49;
Matches 93; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 3 ATROGKPSKRLKARCSKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEPFLSHLEPT 62
DB 85 ASRHGKRGKSKRLKARCSKALHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLSHLEPT 144

QY 63 NHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
DB 145 NHAIVQTLNMSMDPGSTPPSCVPTKLTPI SILYIDAGNNVYKQYEDMVVESCGR 201

RESULT 13
QSKF10 HUMAN PRELIMINARY; PRT; 455 AA.
AC Q6KFI0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Growth differentiation factor 16.
GN Name=GDF6; Synonyms=GDF16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hind brain;
RA Guo J.H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AJ537424; CAD60934.1; -, mRNA.
DR HSP; P01137; IKLA.
DR Ensembl; ENSG00000156466; Homo sapiens.
DR HGNC; HGNC:4221; GDF6.
DR GO; GO:0040007; F: growth factor activity; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta.1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
```

```
SQ SEQUENCE 455 AA; 50661 MW; F9F365B99E8C659C CRC64;

Query Match 83.2%; Score 540; DB 2; Length 455;
Best Local Similarity 79.5%; Pred. No. 1.8e-48;
Matches 93; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 3 ATROGKPSKRLKARCSKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEPFLSHLEPT 62
DB 339 ASRHGKRGKSKRLKARCSKALHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLSHLEPT 398

QY 63 NHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
DB 399 NHAIVQTLNMSMDPGSTPPSCVPTKLTPI SILYIDAGNNVYKQYEDMVVESCGR 455

RESULT 14
O93573 CHICK PRELIMINARY; PRT; 126 AA.
AC O93573;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative growth/differentiation factor 6/7 (Fragment).
GN Name=GDF6/7;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99026113; PubMed=9808626;
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
RT of a discrete class of commissural interneurons in the mouse spinal
RT cord.";
RL Genes Dev. 12:3394-3407(1998).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF089086; AAC97113.1; -, Genomic_DNA.
DR HSP; P08476; INYU.
DR SMR; O93573; 22-126.
DR Ensembl; ENSGALG00000001786; Gallus gallus.
DR GO; GO:0005576; C: extracellular region; IEA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta.1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT NON_TER
SQ SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;

Query Match 82.4%; Score 534.5; DB 2; Length 126;
Best Local Similarity 79.0%; Pred. No. 1.5e-48;
Matches 94; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 2 LATRGKPK-PSKNLKARCSKALHVNFKMGWDDWIIAPLEYEAFHCEGLCEPFLSHLE 60
DB 8 IAAASGGRGHKKAKTRCSRPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLSHLE 67

QY 61 PTNHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
DB 68 PTNHAIVQTLNMSMDPESTPTSCVPSKLSIPISILYIDSGNNVYKQYEDMVVETCGCR 126

RESULT 15
GDF6_BOVIN
ID GDF6_BOVIN STANDARD; PRT; 436 AA.
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AC P55106;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Cartilage-derived
D3 morphogenetic protein 2) (CDMP-2) (Fragment).
GN Name=GDF6; Synonyms=CDMP2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
RA Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.,
RT "Cartilage-derived morphogenetic proteins. New members of the
RT transforming growth factor-beta superfamily predominantly expressed in
RT long bones during human embryonic development.",
RL J. Biol. Chem. 269:28227-28234(1994).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U13661; AAA61416.1; -; mRNA.
DR PIR; B55452; B55452.
DR HSP; P08476; INYU.
DR SMR; P55106; 332-436.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Cytokine; Glycoprotein; Growth factor.
FT PROPEP <1 316 Potential.
FT CHAIN 317 436 Growth/differentiation factor 6.
FT CARBOHYD 27 27 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
FT DISULFID 335 401 By similarity.
FT DISULFID 364 433 By similarity.
FT DISULFID 368 435 By similarity.
FT DISULFID 400 400 Interchain (By similarity).
FT NON_TER 1
SQ SEQUENCE 436 AA; 47873 MW; B0688E12EF8AE91D CRC64;
Query Match 81.4%; Score 528; DB 1; Length 436;
Best-Local Similarity 76.9%; Pred. No. 3.2e-47;
Matches 90; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
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DB 320 ASRHGKRGKSRKLRCSKKPLHVNPKELGWDWIIAPLEYAFHCEGLCEPPLRSHLEPT 379
QY 63 NHAVIQTLMNSMDPEPTTACVPTPLSPISILFLIDSANNVYKQYEDMVVESCGR 119
DB 380 NHAVIQTLMNSMDPGSTPPSCVPTPLSPISILYIDAGNNVYVYEEVYVESCGR 436
Search completed: February 24, 2006, 15:47:25
Job time : 233 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2006, 15:58:53 ; Search time 165 Seconds
(without alignments)
301.344 Million cell updates/sec

Title: US-10-751-451-2

Perfect score: 649

Sequence: 1 PLATQGRKPSNKLKRCR.....ANNVYKQYEDMVESGCR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	645	99.4	119	2	US-08-945-459A-1
2	645	99.4	119	3	US-09-068-253-2
3	645	99.4	119	4	US-10-365-231-1
4	645	99.4	119	4	US-10-414-954-1
5	645	99.4	119	5	US-10-734-583-1
6	645	99.4	120	3	US-09-945-182-4
7	645	99.4	120	4	US-10-779-635-4
8	645	99.4	401	6	US-11-105-344-3
9	645	99.4	501	2	US-08-981-490B-1
10	645	99.4	501	4	US-10-164-279-53
11	645	99.4	501	4	US-10-356-513-1
12	645	99.4	501	4	US-10-356-513-5
13	645	99.4	501	4	US-10-800-917-2
14	645	99.4	501	6	US-11-080-494-1
15	640	98.6	119	3	US-09-880-708-13
16	640	98.6	495	3	US-09-880-708-10
17	639	98.5	502	3	US-09-813-398-37
18	639	98.5	502	5	US-10-826-324-37
19	633	97.5	120	4	US-10-368-345-70
20	629	96.9	501	3	US-09-730-772-13
21	629	96.9	501	3	US-09-735-849-13
22	629	96.9	501	3	US-09-574-819-13
23	629	96.9	501	4	US-10-379-830-13
24	559	86.1	102	4	US-10-800-917-13
25	559	86.1	102	6	US-11-105-344-22
26	548	84.4	354	3	US-09-930-512-74
27	543	83.7	119	4	US-10-693-536-7

28	543	83.7	134	4	US-10-693-536-6
29	540	83.2	120	4	US-10-366-345-69
30	540	83.2	321	3	US-09-945-182-26
31	540	83.2	321	4	US-10-366-345-44
32	540	83.2	321	4	US-10-779-635-26
33	540	83.2	455	3	US-09-825-751A-20
34	540	83.2	455	3	US-09-930-512-20
35	540	83.2	455	4	US-10-297-639-6
36	540	83.2	455	5	US-10-851-438-20
37	538	82.9	263	3	US-09-945-182-32
38	538	82.9	263	4	US-10-779-635-32
39	528	81.4	436	3	US-09-730-772-14
40	528	81.4	436	3	US-09-735-849-14
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43	528	81.4	436	3	US-09-930-512-72
44	528	81.4	436	4	US-10-379-830-14
45	528	81.4	436	4	US-10-164-279-57

ALIGNMENTS

RESULT 1
US-08-945-459A-1
; Sequence 1, Application US/08945459A
; Publication No. US20020102633A1
; GENERAL INFORMATION:
; APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU,
; APPLICANT: HIROYUKI; MIKI, HIDEO; KAWAI,
; APPLICANT: SHINJI; KIMURA, MICHIO; MATSUMOTO,
; APPLICANT: TOMOAKI; KATSUURA, MIEKO; ENOMOTO,
; APPLICANT: KOICHI; SATOH, YUSUKE
; TITLE OF INVENTION: A NOVEL PROTEIN AND
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS
; ADDRESSEE: LLP
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016

COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,459A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/01062
; FILING DATE: 19-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP7/322403
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP7/93664
; FILING DATE: 19-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 AMINO ACIDS
; TYPE: AMINO ACID

STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
ORIGINAL SOURCE:
ORGANISM: HOMOSAPIENS
TISSUE TYPE: FETUS
FEATURE:
NAME/KEY: MP52
LOCATION: 383 TO 501
US-08-945-459A-1

Query Match 99.4%; Score 645; DB 2; Length 119;
Best Local Similarity 99.2%; Pred. No. 2.6e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
DB 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60

QY 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 119
DB 61 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 119

RESULT 2
US-09-068-253-2
Sequence 2, Application US/09068253
Patent No. US2002018381A1
GENERAL INFORMATION:
APPLICANT: SHIMURA, Takesada
APPLICANT: TORIYAMA, Satsuki
TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
FILE REFERENCE: 146.1286
CURRENT APPLICATION NUMBER: US/09/068,253
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: PCT/JP96/03333
PRIOR FILING DATE: 1996-11-14
PRIOR APPLICATION NUMBER: JP 7/322402
PRIOR FILING DATE: 1995-11-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-09-068-253-2

Query Match 99.4%; Score 645; DB 3; Length 119;
Best Local Similarity 99.2%; Pred. No. 2.6e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
DB 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60

QY 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 119
DB 61 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 119

RESULT 3
US-10-365-231-1
Sequence 1, Application US/10365231
Publication No. US20030181378A1
GENERAL INFORMATION:
APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU, HIROYUKI; MIKI, HIDEO; KAWAI, SHINJI; KIMURA, MICHIO; MATSUMOTO, TOMOAKI; KATSUURA, MIEKO; ENOMOTO, KOICHI; SATOH, YUSUKE
TITLE OF INVENTION: A NOVEL PROTEIN AND PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS LLP
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/365,231
FILING DATE: 12-Feb-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01062
FILING DATE: 19-APR-1996
APPLICATION NUMBER: JP7/322403
FILING DATE: 17-NOV-1995
APPLICATION NUMBER: JP7/93664
FILING DATE: 19-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: <Unknown>
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
ORIGINAL SOURCE:
ORGANISM: HOMOSAPIENS
TISSUE TYPE: FETUS
FEATURE:
NAME/KEY: MP52
LOCATION: 383 TO 501
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-365-231-1

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Best Local Similarity 99.2%; Pred. No. 2.6e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
DB 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60

QY 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 119
DB 61 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 119

RESULT 4
US-10-414-954-1
Sequence 1, Application US/10414954
Publication No. US20040019185A1
GENERAL INFORMATION:
APPLICANT: ANDOU, HIDETOSHI
APPLICANT: HONDA, JUN
APPLICANT: SUGIMOTO, SJUNJIRO
APPLICANT: HOTTEN, GETRUD
APPLICANT: BECHTOLD, ROLF
APPLICANT: FOHL, JENS
TITLE OF INVENTION: PROCESS FOR PREPARING PURIFIED ACTIVE MONOMER OF
TITLE OF INVENTION: BONE-DERIVED FACTOR

FILE REFERENCE: 146.1320-1
CURRENT APPLICATION NUMBER: US/10/414,954
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 10/048,458
PRIOR FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/701,121
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PCT/EP00/07600
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 09/331,948
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 10 141379
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: PCT/JP97/04784
PRIOR FILING DATE: 1997-12-24
PRIOR APPLICATION NUMBER: JP 8 355812
PRIOR FILING DATE: 1996-12-25
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human MP52
FEATURE:
NAME/KEY: MOD RES
LOCATION: {83}
OTHER INFORMATION: if dimeric human MP52 variant, Xaa is cysteine; if
OTHER INFORMATION: monomeric human MP52 variant, Xaa is any amino acid
OTHER INFORMATION: except cysteine and preferably alanine, serine,
OTHER INFORMATION: threonine, leucine, isoleucine, glycine or valine
US-10-414-954-1

Query Match 99.4%; Score 645; DB 4; Length 119;
Best Local Similarity 99.2%; Pred. No. 2.6e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRPSKRLKARCSRKALHVNFKDMGWDWIAPLEYAFHCEGLCEFFPLRSHLE 60
Db 1 PLATQGRPSKRLKARCSRKALHVNFKDMGWDWIAPLEYAFHCEGLCEFFPLRSHLE 60

Qy 61 PTNHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 61 PTNHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119

RESULT 5
US-10-734-583-1
Sequence 1, Application US/10734583
Publication No. US20050026247A1
GENERAL INFORMATION:
APPLICANT: Andou, Hidetoshi
APPLICANT: Honda, Jun
APPLICANT: Sugimoto, Shunjiro
APPLICANT: Hotten, Gertrud
APPLICANT: Bechtold, Rolf
APPLICANT: Pohl, Jens
TITLE OF INVENTION: Process for Preparing Purified Active Monomer of Bone-Derived
TITLE OF INVENTION: Factor
FILE REFERENCE: 2923-595
CURRENT APPLICATION NUMBER: US/10/734,583
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: 10/414,954
PRIOR FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 09/331,948
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: PCT/JP97/04784
PRIOR FILING DATE: 1997-12-24
PRIOR APPLICATION NUMBER: 10/048,458
PRIOR FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: PCT/EP00/07600

PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 09/701,121
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PCT/IB99/00866
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: JP 8/355812
PRIOR FILING DATE: 1996-12-25
PRIOR APPLICATION NUMBER: JP 10/141,379
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: EP 99 115 613.4
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: {83}..(83)
OTHER INFORMATION: Xaa = cysteine for producing active dimeric MP52; Xaa = any amino
OTHER INFORMATION: acid preferably except cysteine, and especially preferably
OTHER INFORMATION: alanine, serine, threonine, leucine, isoleucine, glycine or
OTHER INFORMATION: valine for producing active monomeric MP52
US-10-734-583-1

Query Match 99.4%; Score 645; DB 5; Length 119;
Best Local Similarity 99.2%; Pred. No. 2.6e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 PLATQGRPSKRLKARCSRKALHVNFKDMGWDWIAPLEYAFHCEGLCEFFPLRSHLE 60

Qy 61 PTNHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 61 PTNHAIVQTLNMSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119

RESULT 6
US-09-945-182-4
Sequence 4, Application US/09945182
Patent No. US20020160494A1
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,324
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.

REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-945-182-4

Query Match 99.4%; Score 645; DB 3; Length 120;
Best Local Similarity 99.2%; Pred. No. 2.6e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEFPPLRSHLE 60
Db 2 PLATROGKRPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEFPPLRSHLE 61

QY 61 PTNHAVIQTLNMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 62 PTNHAVIQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 120

RESULT 7
US-10-779-635-4
Sequence 4, Application US/10779635
Publication No. US20040146923A1
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/779,635
FILING DATE: 2004-02-18
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: 1997-02-28
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-10-779-635-4

Query Match 99.4%; Score 645; DB 4; Length 120;
Best Local Similarity 99.2%; Pred. No. 2.6e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEFPPLRSHLE 60
Db 2 PLATROGKRPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEFPPLRSHLE 61

QY 61 PTNHAVIQTLNMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 62 PTNHAVIQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 120

RESULT 8
US-11-105-344-3
Sequence 3, Application US/11105344
Publication No. US20050175553A1
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Bechtold, Rolf
APPLICANT: Pohl, Jens
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B FAMILY
FILE REFERENCE: 2923-0286
CURRENT APPLICATION NUMBER: US/11/105,344
CURRENT FILING DATE: 2005-04-14
PRIOR APPLICATION NUMBER: US/09/901,556
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 08/289,222
PRIOR FILING DATE: 1994-08-12
PRIOR APPLICATION NUMBER: DE P 44 23 190.3
PRIOR FILING DATE: 1994-07-01
PRIOR APPLICATION NUMBER: EPO 92102324.8
PRIOR FILING DATE: 1992-02-12
PRIOR APPLICATION NUMBER: PCT/EP93/00350
PRIOR FILING DATE: 1993-02-12
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In version 3.1
SEQ ID NO 3
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
US-11-105-344-3

Query Match 99.4%; Score 645; DB 6; Length 401;
Best Local Similarity 99.2%; Pred. No. 9.8e-60;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEFPPLRSHLE 60
Db 283 PLATROGKRPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEFPPLRSHLE 342

QY 61 PTNHAVIQTLNMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 343 PTNHAVIQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 401

RESULT 9
US-08-981-490B-1
Sequence 1, Application US/08981490B
Publication No. US20020045568A1
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Paulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
FILE REFERENCE: 100564-07032
CURRENT APPLICATION NUMBER: US/08/981,490B

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; CURRENT FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1998-07-12
; PRIOR APPLICATION NUMBER: DE/195 25 416.3
; PRIOR FILING DATE: 1995-07-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-981-490B-1

Query Match          99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.2e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
Db 383 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442

Qy 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
Db 443 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 10
US-10-164-279-53
; Sequence 53, Application US/10164279
; Publication No. US20030185792A1
; GENERAL INFORMATION:
; APPLICANT: Keck, P.
; TITLE OF INVENTION: MORPHOGEN ANALOGS OF BOND MORPHOGENIC PROTEINS
; FILE REFERENCE: CIBT-P04-566
; CURRENT APPLICATION NUMBER: US/10/164,279
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/791946
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-279-53

Query Match          99.4%; Score 645; DB 4; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.2e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
Db 383 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442

Qy 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
Db 443 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 11
US-10-356-513-1
; Sequence 1, Application US/10356513
; Publication No. US20030220248A1
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Pohl, Jens
; APPLICANT: Bechtold, Rolf
; APPLICANT: Paulista, Michael
; APPLICANT: Unsicker, Klaus
; TITLE OF INVENTION: The Use Of MP52 Or MP121 For Treating And Preventing Diseases Of
; FILE REFERENCE: 2923-0127
; CURRENT APPLICATION NUMBER: US/10/356,513
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; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 08/981490
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE 195 25 416 .3
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Human
US-10-356-513-1

Query Match          99.4%; Score 645; DB 4; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.2e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
Db 383 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442

Qy 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
Db 443 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 12
US-10-356-513-5
; Sequence 5, Application US/10356513
; Publication No. US20030220248A1
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Pohl, Jens
; APPLICANT: Bechtold, Rolf
; APPLICANT: Paulista, Michael
; APPLICANT: Unsicker, Klaus
; TITLE OF INVENTION: The Use Of MP52 Or MP121 For Treating And Preventing Diseases Of
; FILE REFERENCE: 2923-0127
; CURRENT APPLICATION NUMBER: US/10/356,513
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 08/981490
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE 195 25 416 .3
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Human
US-10-356-513-5

Query Match          99.4%; Score 645; DB 4; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.2e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
Db 383 PLATQGRKPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442

Qy 61 PTNHAVIOTLMSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
Db 443 PTNHAVIOTLMSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 13
US-10-800-917-2
; Sequence 2, Application US/10800917
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Publication No. US20040146979A1
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF TGF-b Family
FILE REFERENCE: 100564-09022
CURRENT APPLICATION NUMBER: US/10/800,917
CURRENT FILING DATE: 2004-03-16
PRIOR APPLICATION NUMBER: US 08/288,508
PRIOR FILING DATE: 1994-08-10
PRIOR APPLICATION NUMBER: DE P 43 26 829.3
PRIOR FILING DATE: 1993-08-10
PRIOR APPLICATION NUMBER: DE P 44 18 222.8
PRIOR FILING DATE: 1994-05-25
PRIOR APPLICATION NUMBER: DE P 44 20 157.5
PRIOR FILING DATE: 1994-06-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: DOMAIN
LOCATION: (1)..(501)
OTHER INFORMATION: TGF-beta protein MP-52 precursor
US-10-800-917-2

Query Match 99.4%; Score 645; DB 4; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.2e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQKRPKNLKCARKSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEPFLSHLE 60
DB 383 PLATQKRPKNLKCARKSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEPFLSHLE 442

QY 61 PTNHAVIOTLMSMDPESTPPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
DB 443 PTNHAVIOTLMSMDPESTPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 14
US-11-080-494-1
Publication US/11080494
Publication No. US20050169965A1
GENERAL INFORMATION:
APPLICANT: PAULISTA, Michael
APPLICANT: POHL, Jens
TITLE OF INVENTION: COMPOUNDS WITH IMPROVED CARTILAGE-INDUCING AND/OR
TITLE OF INVENTION: BONE-INDUCING ACTIVITY
FILE REFERENCE: 564-9010
CURRENT APPLICATION NUMBER: US/11/080,494
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US/09/297,092
PRIOR FILING DATE: 1999-05-18
PRIOR APPLICATION NUMBER: PCT/EP97/06463
PRIOR FILING DATE: 1997-11-19
PRIOR APPLICATION NUMBER: DE/19647853.7
PRIOR FILING DATE: 1996-11-19
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
US-11-080-494-1

Query Match 99.4%; Score 645; DB 6; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.2e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQKRPKNLKCARKSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEPFLSHLE 60

DB 383 PLATQKRPKNLKCARKSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEPFLSHLE 442

QY 61 PTNHAVIOTLMSMDPESTPPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119

DB 443 PTNHAVIOTLMSMDPESTPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 15
US-09-880-708-13
Sequence 13, Application US/09880708
Patent No. US20020165361A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,708
FILING DATE: 12-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/145,060
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Hallie, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 619/677-1465
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-5
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-880-708-13

Query Match 98.6%; Score 640; DB 3; Length 119;
Best Local Similarity 98.3%; Pred. No. 8.8e-60;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATQKRPKNLKCARKSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEPFLSHLE 60

DB 1 PLATQKRPKNLKCARKSRKALHVNFKDMGDDWIIAPLEYEAFHCEGLCEPFLSHLE 60

QY 61 PTNHAVIOTLMSMDPESTPPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119

DB 61 PTNHAVIOTLMSMDPESTPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119

Search completed: February 24, 2006, 16:02:10
Job time : 168 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions

.rnpbm (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions

.rapbm (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

Inis Page blank (uspto)

GenCore version 5.1.7

Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2006, 15:59:28 ; Search time 18 Seconds
(without alignments)
98.421 Million cell updates/sec

Title: US-10-751-451-2

Perfect score: 649

Sequence: 1 PLATROGKRPSKNLKARCSR.....ANNVYKQYEDMVVSCGCR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/2/pubaa/US05_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/2/pubaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	100.0	119	6	US-10-751-451-2
2	645	99.4	119	7	US-11-191-072-12
3	645	99.4	119	7	US-11-191-072-13
4	645	99.4	501	7	US-11-191-072-2
5	559	86.1	102	6	US-10-816-768-83
6	554	85.4	101	7	US-11-191-072-14
7	510	78.6	102	6	US-10-816-768-85
8	507	78.1	102	6	US-10-816-768-84
9	495	76.3	102	6	US-10-816-768-86
10	494	76.1	203	6	US-10-816-768-100
11	484	74.6	102	6	US-10-816-768-88
12	483	74.4	102	6	US-10-816-768-87
13	353	54.4	129	6	US-10-816-768-89
14	350	53.9	117	6	US-10-816-768-69
15	350	53.9	139	6	US-10-816-768-68
16	347	53.5	396	7	US-11-051-568-5
17	347	53.5	588	6	US-10-650-326B-7
18	339	52.2	408	7	US-11-051-568-7
19	339	52.2	408	7	US-11-124-367A-344
20	339	52.2	408	7	US-11-124-367A-345
21	339	52.2	408	7	US-11-124-367A-346
22	339	52.2	408	7	US-11-124-367A-347
23	339	52.2	419	7	US-11-051-568-19
24	333	51.3	454	6	US-10-650-326B-15
25	332	51.2	513	6	US-10-650-326B-16

26	332	51.2	513	7	US-11-000-463-816	Sequence 816, Appl
27	331.5	51.1	101	6	US-10-816-768-51	Sequence 51, Appl
28	331.5	51.1	101	7	US-11-226-555-10	Sequence 10, Appl
29	331	51.0	102	6	US-10-816-768-45	Sequence 45, Appl
30	330.5	50.9	172	7	US-11-051-568-17	Sequence 17, Appl
31	330	50.8	102	6	US-10-816-768-52	Sequence 52, Appl
32	330	50.8	102	7	US-11-226-555-27	Sequence 27, Appl
33	330	50.8	139	6	US-10-650-326B-1	Sequence 1, Appl
34	330	50.8	139	7	US-11-226-555-5	Sequence 5, Appl
35	330	50.8	317	7	US-11-051-568-11	Sequence 11, Appl
36	330	50.8	408	7	US-11-051-568-15	Sequence 15, Appl
37	330	50.8	431	6	US-10-816-768-39	Sequence 39, Appl
38	330	50.8	431	6	US-10-650-326B-3	Sequence 3, Appl
39	330	50.8	431	7	US-11-051-568-2	Sequence 2, Appl
40	330	50.8	431	7	US-11-186-284-10	Sequence 10, Appl
41	330	50.8	431	7	US-11-226-555-17	Sequence 17, Appl
42	330	50.8	431	7	US-11-192-542A-2	Sequence 2, Appl
43	330	50.8	484	7	US-11-051-568-13	Sequence 13, Appl
44	329	50.7	438	6	US-10-650-326B-9	Sequence 9, Appl
45	328.5	50.6	101	6	US-10-816-768-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-10-751-451-2
; Sequence 2, Application US/10751451
; Publication No. US20060019886A1

GENERAL INFORMATION:

; APPLICANT: Hoechst Marion Roussel
; TITLE OF INVENTION: Novel monomer protein with bone morphogenetic activity
; TITLE OF INVENTION: and medicinal agent containing the same for preventing
; TITLE OF INVENTION: and treating diseases of cartilage and bone.
; FILE REFERENCE: JH98K008 PCT SEQUENCES IN ENGLISH
; CURRENT APPLICATION NUMBER: US/10751.451
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US/09/701,121
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 10-141379
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 2

LENGTH: 119

TYPE: PRT

ORGANISM: HUMAN

US-10-751-451-2

Query Match 100.0%; Score 649; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 9e-67;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLATROGKRPSKNLKARCSRKALHVNFKDGDWDIIAPLEYAFHCEGLCEFLRSHLE 60

Db 1 PLATROGKRPSKNLKARCSRKALHVNFKDGDWDIIAPLEYAFHCEGLCEFLRSHLE 60

Qy 61 PTNHAVTQTLNMSNDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119

Db 61 PTNHAVTQTLNMSNDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119

RESULT 2

US-11-191-072-12

; Sequence 12, Application US/11191072

; Publication No. US20050282255A1

GENERAL INFORMATION:

; APPLICANT: Hotten, Gertrud
; APPLICANT: Bechtold, Rolf
; APPLICANT: Pohl, Jens
; TITLE OF INVENTION: Monomeric Protein of the TGF-beta Family
; FILE REFERENCE: 2923-128
; CURRENT APPLICATION NUMBER: US/11/191.072

```

; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/10/048,458
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: PCT/EP00/07600
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: EP 99115613.4
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutated recombinant human MP52
US-11-191-072-12

Query Match          99.4%; Score 645; DB 7; Length 119;
Best Local Similarity 99.2%; Pred. No. 2.5e-66;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
   |||||||
Db 1 PLATQGRKPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
   |||||||

QY 61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
   |||||||
Db 61 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
   |||||||

RESULT 3
US-11-191-072-13
; Sequence 13, Application US/11191072
; Publication No. US20050282255A1
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Bechtold, Rolf
; APPLICANT: Pohl, Jens
; TITLE OF INVENTION: Monomeric Protein of the TGF-beta Family
; FILE REFERENCE: 2923-128
; CURRENT APPLICATION NUMBER: US/11/191,072
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/10/048,458
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: PCT/EP00/07600
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: EP 99115613.4
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 13
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: monomeric mutated recombinant human MP52
; NAME/KEY: MISC FEATURE
; LOCATION: (83)-(83)
; OTHER INFORMATION: Xaa = any amino acid except cysteine
US-11-191-072-13

Query Match          99.4%; Score 645; DB 7; Length 119;
Best Local Similarity 99.2%; Pred. No. 2.5e-66;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
   |||||||
Db 1 PLATQGRKPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
   |||||||

QY 61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
   |||||||
Db 61 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
   |||||||
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RESULT 4

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US-11-191-072-2
; Sequence 2, Application US/11191072
; Publication No. US20050282255A1
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Bechtold, Rolf
; APPLICANT: Pohl, Jens
; TITLE OF INVENTION: Monomeric Protein of the TGF-beta Family
; FILE REFERENCE: 2923-128
; CURRENT APPLICATION NUMBER: US/11/191,072
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/10/048,458
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: PCT/EP00/07600
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: EP 99115613.4
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (465)..(465)
; OTHER INFORMATION: Xaa = any amino acid
US-11-191-072-2

Query Match          99.4%; Score 645; DB 7; Length 501;
Best Local Similarity 99.2%; Pred. No. 1.3e-65;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
   |||||||
Db 383 PLATQGRKPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLE 442
   |||||||

QY 61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
   |||||||
Db 443 PTNHAVIQTLMNSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 501
   |||||||
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RESULT 5

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US-10-816-768-83
; Sequence 83, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 2.0
; SEQ ID NO 83
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CDM-1/GDF-5
US-10-816-768-83

Query Match          86.1%; Score 559; DB 6; Length 102;
Best Local Similarity 99.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEFFPLRSHLEPTNHAVIQTLMNSMDPE 77
   |||||||
```

Db 1 CSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPE 60
QY 78 STPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 61 STPTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 102

RESULT 6

US-11-191-072-14
; Sequence 14, Application US/11191072
; Publication No. US20050282255A1
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Bechtold, Rolf
; APPLICANT: Pohl, Jens
; TITLE OF INVENTION: Monomeric Protein of the TGF-beta Family
; FILE REFERENCE: 2923-128
; CURRENT APPLICATION NUMBER: US/11/191,072
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/10/048,458
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: PCT/EP00/07600
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: EP 99115613.4
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (66)..(66)
; OTHER INFORMATION: Xaa = any amino acid except cysteine
US-11-191-072-14

Query Match 85.4%; Score 554; DB 7; Length 101;
Best Local Similarity 99.0%; Pred. No. 4.4e-56;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPE 77
Db 1 CSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPE 60
QY 78 STPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 118
Db 61 STPTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 101

RESULT 7

US-10-816-768-85
; Sequence 85, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 85
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: GDF-6
US-10-816-768-85

Query Match 78.6%; Score 510; DB 6; Length 102;

Best Local Similarity 85.3%; Pred. No. 4.4e-51;
Matches 87; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
QY 18 CSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPE 77
Db 1 CSRKALHVNFKELGWDDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPG 60
QY 78 STPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 61 STPTCCVPTRLTPISILYIDAGNNVVKQYEDMVVESCGR 102

RESULT 8

US-10-816-768-84
; Sequence 84, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 84
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CDMF-2/GDF-6
US-10-816-768-84

Query Match 78.1%; Score 507; DB 6; Length 102;
Best Local Similarity 84.3%; Pred. No. 9.6e-51;
Matches 86; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

QY 18 CSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPE 77
Db 1 CSRKALHVNFKELGWDDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPG 60
QY 78 STPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 61 STPTCCVPTRLTPISILYIDAGNNVVKQYEDMVVESCGR 102

RESULT 9

US-10-816-768-86
; Sequence 86, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 86
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: CDMF-2
US-10-816-768-86

Query Match 76.3%; Score 495; DB 6; Length 102;
Best Local Similarity 81.4%; Pred. No. 2.2e-49;
Matches 93; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

Db 81 VHFNPETVPKCCAPTQLSAIVLYFDSSNVILKYYEDMVVEACGCR 129

RESULT 14

US-10-816-768-69
; Sequence 69, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Trypsin truncated H2223 mutant
US-10-816-768-69

Query Match 53.9%; Score 350; DB 6; Length 117;
Best Local Similarity 51.4%; Pred. No. 7.1e-33;
Matches 56; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

Qy 11 SKNLKARCSRKALHVNFKDMGDDWIIAPLEYEAHFHCEGLCEFPPLRSHLEPTNHAVIOTL 70

Db 9 SSDQRQACKKHELIVSFRDLGQDWIIAPEGYAAAYCEGCAFFPLNSYMNATNHAIQVTL 68

Qy 71 MNSMDPESTPTTACVPTRLSPISILFIDSANNVVKYQEDMVVESCGR 119

Db 69 VHFNPETVPKCCAPTQLSAIVLYFDSSNVILKYYEDMVVEACGCR 117

RESULT 15

US-10-816-768-68
; Sequence 68, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 68
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature H2223 mutant
US-10-816-768-68

Query Match 53.9%; Score 350; DB 6; Length 139;
Best Local Similarity 51.4%; Pred. No. 8.7e-33;
Matches 56; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

Qy 11 SKNLKARCSRKALHVNFKDMGDDWIIAPLEYEAHFHCEGLCEFPPLRSHLEPTNHAVIOTL 70

Db 31 SSDQRQACKKHELIVSFRDLGQDWIIAPEGYAAAYCEGCAFFPLNSYMNATNHAIQVTL 90

Qy 71 MNSMDPESTPTTACVPTRLSPISILFIDSANNVVKYQEDMVVESCGR 119

Db 91 VHFNPETVPKCCAPTQLSAIVLYFDSSNVILKYYEDMVVEACGCR 139

Search completed: February 24, 2006, 16:02:32
Job time : 19 secs

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